

REMARKS

1. Information Disclosure Statement

The Examiner notes that the IDS filed March 24, 2004 "contains 2 pages of form PTO-892 from the parent application that have been lined through. This fails to comply with 37 CFR 1.98(a)(1)... The information disclosure statement has been placed in the application file, but the information referred to therein has not been considered".

Our file copy for this case has two pages of 892s from the prior case (one listing Bork the other Witkowski, as the first reference), but neither page has any lined through text (copy enclosed). It therefore seems to us is that if these forms were lined through, it happened at the PTO after we filed this case, and we are not responsible for same.

Moreover, these 892s are clearly compliant (if not lined through by applicant) with 37 CFR 1.98(a)(1). When an IDS is filed with an application, as it was in this case, it is clearly not possible to place, on each page of the IDS, the serial number of the application in which the IDS is being submitted, because the serial number is not yet assigned. The 892 forms in question segregate US patents from citations of other documents, provide a column for the application, and have a heading that clearly indicates that the list is an IDS ("Notice of References Cited").

Without conceding that the 892s were in any way non-compliant, to facilitate prosecution counsel has now added, to the enclosed copies, the words "INFORMATION DISCLOSURE STATEMENT" and the now-known serial number of this case (10/807,115) and requests that the references be considered.

2. Written Description

Claims 1-10 and 12-19 stand rejected under the written description requirement of 35 USC 112, para. 1. We traverse.

Claim 1 is directed to

1. An isolated or non-naturally occurring DNA construct, the nucleic acid sequence of which comprises (I) a coding sequence coding for an

expressible protein which is (a) a pre-prochymosin, prochymosin, or chymosin of a mammal of the suborder Tylopoda or (b) a fusion protein comprising a core protein, wherein said fusion protein is cleavable to release said core protein and wherein said core protein is such a pre-prochymosin, prochymosin or chymosin; and
(II) appropriate expression signals, operably linked to said coding sequence, permitting the protein to be expressed in a host cell.

Claim 2 limits the mammal to genus Camelus, and claim 3, to the species Camelus dromedaries.

Claim 5 is a method of producing the tylopodal protein encoded by the DNA of claim 1, and is limited by claim 6 to a Camelus dromedaries protein and by claim 19 to the genus Camelus.

Claims 10 and 11 recite

10. The method of claim 5 wherein the DNA construct is identical to pGAMpR except that said DNA construct comprises a different coding sequence.

11. The method of claim 10 wherein the DNA construct is pGAMpR-C as contained in the *Aspergillus niger* var. *awamori* strains deposited under the accession numbers CBS 108915 and CBS 108916.¹

The Examiner states

Suborder of Tylopoda comprises various mammals. The genus of *Camelus* comprises various species including *Camelus dromedaries*. In a given species chymosin can be encoded by single or different genes. (i.e., the claim covers all allelic variants of the chymosin gene in each species).

The Examiner opines that "the claims are drawn to a large highly diverse genus of nucleic acid sequences from Tylopoda, Camelus or Camelus dromedaries encoding pre-prochymosin, prochymosin, or chymosin".

The Examiner concedes that the specification discloses, as

¹ We have amended 11 to make it dependent on 5, not 10, since 10 expressly is not identical to pGAMpR.

a representative example of the claimed genus of DNA constructs, "a single plasmid pGAMpR-C containing Camelus dromedaries gene coding for chymosin (pages 18-19, Example 1).

The Examiner says that the legal standard for written description is, per Eli Lilly:

To fully describe a genus of genetic material, which is a chemical compound, applicants must (1) fully describe at least one species of the claimed genus sufficient to represent said genus whereby a skilled artisan, in view of the prior art, could predict the structure of other species encompassed by the claimed genus and (2) identify the common characteristics of the claimed molecules, e.g., structure, physical and/or chemical characteristics, functional characteristics when coupled with a known or disclosed correlation between function and structure, or a combination of these.

We agree with this statement of the law, but believe it has been misapplied here.

We first address the issue of taxonomic diversity. The suborder Tylopoda is divided into four families: Xiphodontidae, Protoceratidae, Oromerycidae, and camelidae. The first three families are extinct and hence are irrelevant to the patentability issues.

The family Camelidae in turn consists of three genera, and a total of six species, as follows

Llama

- L. glama (llama)
- L. guanicoe (Guanaco)

Vicugna

- V. vicugna (Vicuña)
- V. pacos (Alpaca)
- (formerly classified as L. pacos)

Camelus

- C. dromedaries (Dromedary)
- C. bactrianus (Bactrian Camel).

We don't think that a taxon consisting of merely six living species (Tylopoda) or two living species (Camelus) can be

considered "diverse", let alone large and, highly diverse, absent some prima facie showing by the examiner.

Prochymosin sequences for the six species in question have not been published, but the inventors have obtained the complete sequences for C. dromedaries, C. bactrianus and L. llama, and a partial sequence for L. guanicoe.

The table below compiles the amino acid identity of these four species with each other and with Bos taurus and water buffalo:

	Bos taurus	water buffalo	C. bactrianus	C. dromedarius	Llama	Guanaco
Bos taurus	100	94	83	84	84	86
water buffalo		100	79	80	80	84
C. bactrianus			100	98	97	96
C. dromedarius				100	98	96
Llama					100	96
Guanaco						100

It can be seen that the tylopodal prochymosins have a sequence identity among themselves which lies in the 98% range, but are only 80-93% identical to Bos taurus, and 79-84% identical to water buffalo.

We respectfully direct the Examiner's attention to the Example 14 in the PTO's Revised Written Description Guideline Training Materials:

There is actual reduction to practice of the single disclosed species [SEQ ID NO:3]. The specification indicates that the genus of proteins that must be variants of SEQ ID NO: 3 does not have substantial variation since all of the variants must possess the specified catalytic activity and must have at least 95% identity to the reference sequence, SEQ ID NO: 3. The single species disclosed is representative of the genus

because all members have at least 95% structural identity with the reference compound and because of the presence of an assay which applicant provided for identifying all of the at least 95% identical variants of SEQ ID NO: 3 which are capable of the specified catalytic activity. One of skill in the art would conclude that applicant was in possession of the necessary common attributes possessed by the members of the genus.

While claim 1 doesn't use explicit percentage sequence identity language, it is clear that the tylopodal chymosins in fact share at least 95% sequence identity. The term "chymosin" implies a particular biological activity. Hence, claim 1 is within the purview of RWDGTM Ex. 14.

It is also interesting to note that when these sequences are aligned with each other and bovine chymosin (see Figures A and B attached), there are three areas of special interest:

- a.a. 57-68, with 6 *Tylopoda* specific amino acids. The differences between *Tylopoda* and bovine chymosin in this area result in a remarkable change in charge. These comprise the first amino acids of the mature chymosin molecule.
- a.a 160-161. Two very exposed amino acid residues at the backbone of the molecule.
- a.a 301-329. Most differences between *Tylopoda* and bovine prochymosins are located at the C-terminal part of the molecule. The 301-329 area is located at the entrance of the catalytical cleft and is likely to be responsible for interaction with the casein substrate of the molecule.

Most differences from bovine chymosin are found in all four *Tylopoda* species analyzed. There are only two cases in which both *Camelus* sequences differ from the two *Llama* sequences (in both cases the *Camelus* chymosins have an 'R' while the *Llama* chymosins have H in one case and Q in the other case).

Based on this comparison it is unlikely that major differences will be found in the functional properties of different *Tylopoda* chymosin molecules.

Even absent knowledge of the tylopodal chymosin sequences, it would have been expected that they are similar in structure, given the overall similarity seen for other tylopodal proteins.

There are only a few proteins for which published sequences are available for the three tylopodal genera, Camelus, Llama and Vicugna (see Exs. C-F).

The first is cytochrome b. Using a Camelus dromedarius sequence (P24952) as the query sequence, we found the following BLAST search results (Ex. G)²

	<u>Identity</u>	<u>Similarity</u>
C. bactrianus (Q34028)	97	98
L. glama (Q5GH08)	94	97
L. guanicoe (Q5GH04)	94	97
V. vicugna (Q5GH07)	93	96
L. pacos (Q5G115)	93	96
Sus philippensis (Q5BQG9) (highest-ranked non-tylopodal)	90	95

We see that at least the Cameuls genus cytochrome b proteins have within- taxon identity exceeding 95% and the tylopodal proteins generally are at least 93% identical to C. dromedarius. Cytochrome b being a housekeeping protein, it is pretty well conserved even across a broader taxonomic

² BLAST search, without low-complexity filtering since that corrupts the percent identity calculation.

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distance.

Then we have hemoglobin alpha and beta chain; searching with a C. dromedarius sequence alpha (P63106) (Ex. H) and beta (P68231) (Ex. I) we get:

	vs. C. dromedarius Hemoglobin A chain (P63106)		vs. C. dromedarius Hemoglobin B chain (P68231)	
	<u>Identity</u>	<u>Similarity</u>	<u>Identity</u>	<u>Similarity</u>
C. bactrianus	100 (P63105)	100	100 (P68230)	100
L. pacos	97 (P67816)	99	98 (P68228)	100
L. guanicoe	97 (P67815)	99	98 (P68229)	100
L. vicugna	97 (P07425)	98	98 (P68227)	100
L. glama	96 (P01973)	98	98 (P68226)	100
Colobus badius (best non-tylopodal hit for Hgb-alpha)	87 (P01930)	92		
Ailuropoda melanoleuca (best non-tylopodal hit for Hgb-beta)			86 (P18983)	93

Again, we see that the tylopodal globin proteins have within-taxon identities of over 95%.

Additional examples could be provided. While we don't have comparative sequence data on other tylopodal milk proteins it is interesting to note that for alpha-1 casein and beta casein, the best non-tylopodal matches to C. dromedarius have 47% (Ex. J) and 67% (Ex. K) identity, respectively.

Clearly, the art would consider a Camelus dromedarius protein to be representative of its tylopodal homologues.

As to allelic variation of the chymosin gene within the species Camelus dromedaries, the Examiner has not made a prima facie showing that the degree of allelic variation is or would

have been expected to be so great that the particular sequence embodied in pGAMpR-C would not be representative of all C. dromedaries chymosins. In this regard, note that for the proteins for which multiple C. dromedaries isolates have been sequenced, the isolated have all been at least 95% identical, and often completely identical, with the query sequence.

Enablement

1. The Examiner contends that the claims are enabling only for a nucleic acid sequence encoding chymosin contained in pGAMpR-C.

While recombinant hybridization techniques are known, only highly homologous sequences can be identified using a given sequence. The state of the art provides no reasonable expectation of success in obtaining a nucleic acid sequence from Tylopoda, *Camelus*, or another gene of *Camelus dromedaries* and the result of such screening is unpredictable.

It is clear from the showing made in connection with written description that the tylopodal proteins would have been expected to be highly homologous and are indeed highly homologous.

The literature shows that it is possible to use a gene of one species as a hybridization probe to isolate the homologous gene of another species even when the corresponding proteins have amino acid identities of less than 95%.

For the use of probes to successfully identify homologous genes in other species, see, e.g., Schwinn, et al., J. Biol. Chem., 265:8183-89 (1990) (hamster 67-bp cDNA probe vs. human leukocyte genomic library; human 0.32kb DNA probe vs. bovine brain cDNA library, both with hybridization at 42°C in 6xSSC); Jenkins et al., J. Biol. Chem., 265:19624-31 (1990) (Chicken 770-bp cDNA probe vs. human genomic libraries; hybridization at 40°C in 50% formamide and 5xSSC); Murata et al., J. Exp. Med., 175:341-51 (1992) (1.2-kb mouse cDNA probe v. human

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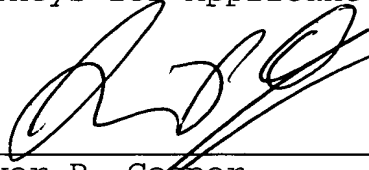
eosinophil cDNA library; hybridization at 65°C in 6xSSC); Guyer et al., J. Biol. Chem., 265:17307-17 (1990) (2.95-kb human genomic DNA probe vs. porcine genomic DNA library; hybridization at 42°C in 5xSSC).

Since the tylopodal proteins have identities exceeding 95% it would not, and indeed did not, require undue experimentation to isolate chymosin genes of *C. bactrianus*, *L. llama* and *L. guanicoe* using the *C. dromedaries* sequence from pGAMpR-C as a probe. Likewise, it would not require undue experimentation to likewise isolate chymosin genes of *V. vicugna* or *V. pacos*.

2. In response to OA page 7, Applicants hereby states for the record that CBS 108915 and 108916 were deposited on June 13, 2000 under the Budapest Treaty, and will be made available in compliance with 37 CFR 1.801-1.809.

Respectfully submitted,

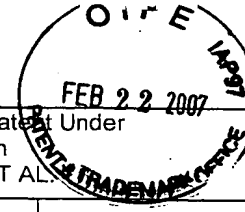
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Enclosures

- copies of previously filed 892s, marked-up as described in section 1 of response
- Figures A and B
- Exhibit C: *Camelus bactrianus* proteins with known sequences
- Exhibit D: *Llama* proteins with known sequences
- Exhibit E: *Vicugna* proteins with known sequences
- Exhibit F: *Camelus dromedarius* proteins with known sequences
- Exhibits G-K: BLAST search results

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INFORMATION DISCLOSURE STATEMENT Notice of References Cited	Application/Control No. 10/807,115	Applicant(s)/Patent Under Reexamination KAPPELER ET AL.	
	Examiner Delia M. Ramirez	Art Unit 1652	Page 1 of 2

U.S. PATENT DOCUMENTS

*		Document Number Country Code-Number-Kind Code	Date MM-YYYY	Name	Classification
	A	US-			
	B	US-			
	C	US-			
	D	US-			
	E	US-			
	F	US-			
	G	US-			
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	M	US-			

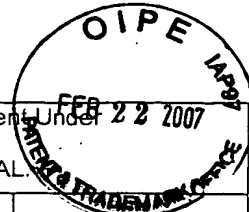
FOREIGN PATENT DOCUMENTS

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	N					
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	P					
	Q					
	R					
	S					
	T					

NON-PATENT DOCUMENTS

*		Include as applicable: Author, Title Date, Publisher, Edition or Volume, Pertinent Pages)
	U	Bork , Genome Research, 10:398-400, 2000.
	V	Broun et al. , Science 282:1315-1317, 1998.
	W	Van de Loo et al. , Proc. Natl. Acad. Sci. 92:6743-6747, 1995.
	X	Seffernick et al. , J. Bacteriol. 183(8):2405-2410, 2001.

*A copy of this reference is not being furnished with this Office action. (See MPEP § 707.05(a).)
Dates in MM-YYYY format are publication dates. Classifications may be US or foreign.



INFORMATION DISCLOSURE STATEMENT
Notice of References Cited

Application/Control No.

10/807,115

Applicant(s)/Patent Under

Reexamination
KAPPELER ET AL.

Examiner

Delia M. Ramirez

Art Unit

1652

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FOREIGN PATENT DOCUMENTS

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	R					
	S					
	T					

NON-PATENT DOCUMENTS

*		Include as applicable: Author, Title Date, Publisher, Edition or Volume, Pertinent Pages)
	U	Witkowski et al. , Biochemistry 38:11643-11650, 1999.
	V	Nomura et al. , Appl. Microbiol. Biotechnol. 42:865-870, 1995.
	W	Pungercar et al. , Nucleic Acids Research 18(15):4602, 1990
	X	

*A copy of this reference is not being furnished with this Office action. (See MPEP § 707.05(a).)
Dates in MM-YYYY format are publication dates. Classifications may be US or foreign.

Figure A, comparison of bovine prochymosin with prochymosins from different *Tylopoda* species. Aminoacids indicated with bold and blue in the consensus sequence are conserved within the *Tylopoda* family but absent in the bovine family. *Tylopoda* specific sequence motifs with a potential structural function have been underlined in the consensus sequence.

50		
Bos bovis chymosin B	(1)	MRCLVLLAVFALSQGAETRIPLYKGKSLRKALKEHGLLEDFLQKQQYG
Water buffalo	(1)	-----MAEITRIPLCKGKSLRKALKEHGLLEDFLQKQQYG
Camelus dromedarius	(1)	MRCLVLLAALALSQASGITRIPLHKGKTLRKALKERGLLEDFLQKQQYA
C. bactrianus	(1)	MRCLVLLAALALSQASGITRIPLHKGKTLRKALKERGLLEDFLQKQQYA
guanaco	(1)	-----IPLYKGKTLRKALKEHGLLEDFLQKQQYA
Llama	(1)	MRCLVLLAALALSQASGITRIPLYKGKTLRKALKEHGLLEDFLQKQQYA
Consensus	(1)	MRCLVLLAALALSQASGITRIPLYKGK <u>TLRKALKEHGLLEDFLQKQQYA</u>
	51	100
Bos bovis chymosin B	(51)	ISSKYSGFGEVASVPLTNYLDSQYFGKIYLGTPPQEFTVLFDTGSSDFWV
Water buffalo	(36)	VSSKYSGFGEVASVPLTNYLDSQYFGKIYLGTPPQEFTVLFDTGSSDFWV
Camelus dromedarius	(51)	VSSKYSSLGKVAREPLTSYLDQYFGKIYIGTPPQEFTVVFDTGSSDLWV
C. bactrianus	(51)	VSSKYSSLGKVAREPLTSYLDQYFGKIYIGTPPQEFTVVFDTGSSDLWV
guanaco	(30)	VSSKYSSLGKVAREPLTSYLDQYFGKIYIGTPPQEFTVVFDTGSSDLWV
Llama	(51)	VSSKYSSLGKVAREPLTSYLDQYFGKIYIGTPPQEFTVVFDTGSSDLWV
Consensus	(51)	VSSKYSS <u>SLGKVAREPLTS</u> YLDQYFGKIYIGTPPQEFTVVFDTGSSDLWV
	101	150
Bos bovis chymosin B	(101)	PSIYCKSNACKNHQRFDP---RKSSTFQNLGKPLSIHYGTGSMQGILGYD
Water buffalo	(86)	PSIYCKSNACKNHQRFDP---RKSSTFQNLGKPLSIRYGTGSMQGILGYD
Camelus dromedarius	(101)	PSIYCKSNVCKNHHRFDP---RKSSTFRNLGKPLSIHYGTGSMGFLGYD
C. bactrianus	(101)	PSIYCKSNACKNHHRFDP---RKSSTFRNLGKPLSIHYGTGSMGFLGYD
guanaco	(80)	PSIYCKSNACXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
Llama	(101)	PSIYCKSNVCKNHHRFDP---RKSSTFRNLGKPLSIHYGTGSMGFLGYD
Consensus	(101)	PSIYCKSNACKNHHRFDPXXRKSST <u>FRNLGKPLSIHYGTGSMGFLGYD</u>
	151	200
Bos bovis chymosin B	(148)	TVTNSNIVDIQQTVGLSTQEPGDVFTYAEFDGILGMAYPSLASEYSIPVF
Water buffalo	(133)	TATVSNIVDIQQTVGLSTQEPGDVFTYAEFDGILGMAYPSLASEYSIPVF
Camelus dromedarius	(148)	TVTNSNIVDPNQTVGLSTEQPGEVFTYSEFDGILGLAYPSLASEYSVPVF
C. bactrianus	(148)	TVTNSNIVDPNQTVGLSTEQPGEVFTYSEFDGILGLAYPSLASEYSVPVF
guanaco	(130)	XXXVSNIVDPNQTVGLSTEQPGEVFTYSEFDGILGLAYPSLASEYSVPVF
Llama	(148)	TVTNSNIVDPNQTVGLSTEQPGEVFTYSEFDGILGLAYPSLASEYSVPVF
Consensus	(151)	TVTNSNIVD <u>PNQTVGLSTEQPGEVFTYSEFDGILGLAYPSLASEYSVPVF</u>
	201	250
Bos bovis chymosin B	(198)	DNMMNRHLVAQDLFSVYMDRNGQESMLTLGAIDPSYTTGSLHWVPVTVQQ
Water buffalo	(183)	DNMMNRHLVAQDLFSVYMDRNGQESMLTLGAIDPSYTTGSLHWVPVTVQQ
Camelus dromedarius	(198)	DNMMDRHLVARDLFSVYMDRNGQGSMLTLGAIDPSYTTGSLHWVPVTLQQ
C. bactrianus	(198)	DNMMDRHLVARDLFSVYMDRNGQGSMLTLGATDPSYTTGSLHWVPVTVQQ
guanaco	(180)	DNMMDRHLVAQDLFSVYMDXXXXXXXXXXXXXXXXXXXXXXXXXXXX
Llama	(198)	DNMMDRHLVAQDLFSVYMDRNGQGSMLTLGAIDSSYTTGSLHWVPVTVQQ
Consensus	(201)	DNMMDRHLVAQDLFSVYMDRNGQGSMLTLGAIDPSYTTGSLHWVPVTVQQ
	251	300
Bos bovis chymosin B	(248)	YWQFTVDSVTISGVVVACEGGCQAILDTGTSKLVGPSSDILNIQQAIGAT
Water buffalo	(233)	YWQFTVDSITISGVVVACEGGCQAILDTGTSKLVGPSSDILNIQQAIGAT
Camelus dromedarius	(248)	YWQFTVDSVTINGVAVACVGGCQAILDTGTSVLFGPSSDILKIQMAIGAT
C. bactrianus	(248)	YWQFTVDSVTINGVAVACVGGCQAILDTGTSVLFGPSSDILKIQMAIGAT
guanaco	(230)	XXXXXXXXVTINGVAVACVGGCQAILDTGTSVLFGPSSDILKIQMAIGAT
Llama	(248)	YWQFTVDSVTINGVAVACVGGCQAILDTGTSVLFGPSSDILKIQMAIGAT
Consensus	(251)	YWQFTVDSVTINGVAVACVGGCQAILDTGT <u>SVLFGPSSDILKIQMAIGAT</u>
	301	350
Bos bovis chymosin B	(298)	QNQYGEFDIDCDNLSYMPTVVFEINGKMYPLTPSAYTSQDQGFCTSGFQS
Water buffalo	(283)	QNQYGEFDIDCDNLSYMPTVVSEINGKMYPLTPSAYTSQDQGFCTSGFQS
Camelus dromedarius	(298)	ENRYGEFDVNCNLRSMPTVVFEINGRDYPLSPAYTSKDQGFCTSGFQG
C. bactrianus	(298)	ENRYGEFDVNCGLRSMPTVVFEINGRDFPLAPAYTSKDQGFCTSGFQG
guanaco	(280)	ENRYGEFDVNCNLRSMPTVVFEINGRDFPLAPAYTSKDQGFCTSGFQS

Llama	(298)	ENRYGEFDVNCGNLRSMPTVVFEINGRDYPLSPSAYTSKDQGFCTSGFQG
Consensus	(301)	<u>ENRYGEFDVNCGNLRSMPTVVFEINGRDYPLSPSAYTSKDQGFCTSGFQS</u>
	351	384
Bos bovis chymosin B	(348)	ENHSQKWILGDVFIREFYYSVFDRAANNLVGLAKAI
Water buffalo	(333)	ENRSQQWILGDVFIREFYYSVFDRAANNLVGLAKAI
Camelus dromedarius	(348)	DNNSELWILGDVFIREFYYSVFDRAANNRVGLAKAI
C. bactrianus	(348)	DNNSELWILGDVFIREFYYSVFDRAANNRVGLAKAI
guanaco	(330)	ENHSQKWILGDVFIREFYYSVFDRAANNLVGLAKAI
Llama	(348)	DNNSELWILGDVFIREFYYSVFDRAANNRVGLAKAI
Consensus	(351)	DNNSQLWILGDVFIREFYYSVFDRAANNRVGLAKAI

Figure B, Comparison of the amino acid sequence of bovine, porcine and Tylopoda prochymosins

			50		
Bos_bovis_chymosin_B	MRCLVLLAV	FALSQGAET	RIPLYKGKSL	RKALKEHGLL	EDFLQKQQYG
C._bactrianus	MRCLVLLAA	LALSQASGIT	RIPLHKGKTL	RKALKERGLL	EDFLQRQQYA
Camelus_dromedarius	MRCLVLLAA	LALSQASGIT	RIPLHKGKTL	RKALKERGLL	EDFLQRQQYA
Lama	MRCLVLLAA	LALSQASGIT	RIPLYKGKTL	RKALKEHGLL	EDFLQRQQYA
Pig	.IRGRVLLAV	LALSQSGGIT	RVPLRKGKSL	RKELKERGLL	EDFLQKQPYA
		51			100
Bos_bovis_chymosin_B	ISSKYSGFGE	VASVPLTNYL	DSQYFGKIYL	GTPPQEFTVL	FDTGSSDFWV
C._bactrianus	VSSKYSSLGK	VAREPLTSYL	DSQYFGKIYI	GTPPQEFTVV	FDTGSSDLWV
Camelus_dromedarius	VSSKYSSLGK	VAREPLTSYL	DSQYFGKIYI	GTPPQEFTVV	FDTGSSDLWV
Lama	VSSKYSSLGK	VAREPLTSYL	DSQYFGKIYI	GTPPQEFTVV	FDTGSSDLWV
Pig	LSSKYSSFGE	VASEPLTNYL	DTQYFGKIYI	GTPPQEFTVV	FDTGSSELWV
		101			150
Bos_bovis_chymosin_B	PSIYCKSNAC	KNHQRFDPRK	SSTFQNLGKP	LSIHYGTGSM	QGILGYDTVT
C._bactrianus	PSIYCKSNAC	KNHHRFDPRK	SSTFRNLGKP	LSIHYGTGSI	EGFLGYDTVT
Camelus_dromedarius	PSIYCKSNVC	KNHHRFDPRK	SSTFRNLGKP	LSIHYGTGSM	EGFLGYDTVT
Lama	PSIYCKSNVC	KNHHRFDPRK	SSTFRNLGKP	LSIHYGTGSM	EGFLGYDTVT
Pig	PSVYCKSDAC	QNHHRFNPSK	SSTFQNLDKP	LSIQYGTGSI	QGFLGYDTVM
		151			200
Bos_bovis_chymosin_B	VSNIVDIQQT	VGLSTQEPGD	VFTYAEFDGI	LGMAYPSLAS	EYSIPVFDNM
C._bactrianus	VSNIVDPNQT	VGLSTEQPGE	VFTYSEFDGI	LGLAYPSLAS	EYSVPVFDNM
Camelus_dromedarius	VSNIVDPNQT	VGLSTEQPGE	VFTYSEFDGI	LGLAYPSLAS	EYSVPVFDNM
Lama	VSNIVDPNQT	VGLSTEQPGE	VFTYSEFDGI	LGLAYPSLAS	EYSVPVFDNM
Pig	VAGIVDAHQT	VGLSTQEPGD	IFTYSEFDGI	LGLGYPELAS	EYTVPVFDNM
		201			250
Bos_bovis_chymosin_B	MNRHLVAQDL	FSVYMDRNGQ	ESMLTLGAID	PSYYTGSLSHW	VPVTVQQYWQ
C._bactrianus	MDRHLVARDL	FSVYMDRNGQ	GSMLTLGATD	PSYYTGSLSHW	VPVTVQQYWQ
Camelus_dromedarius	MDRHLVARDL	FSVYMDRNGQ	GSMLTLGAID	PSYYTGSLSHW	VPVTLQQYWQ
Lama	MDRHLVAQDL	FSVYMDRNGQ	GSMLTLGAID	SSYYTGSLSHW	VPVTVQQYWQ
Pig	MHRHLVAQDL	FAVYMSRNDE	GSMLTLGAID	PSYYTGSLSHW	VPVTMLQYWQ
		251			300
Bos_bovis_chymosin_B	FTVDSVTISG	VVACVGGCQ	AILDGTGTSKL	VGPSSDILNI	QQAIGATQNQ
C._bactrianus	VTVDVSTING	VAVACVGGCQ	AILDGTGTSVL	FGPSSDILKI	QMAIGATENR
Camelus_dromedarius	FTVDSVTING	VAVACVGGCQ	AILDGTGTSVL	FGPSSDILKI	QMAIGATENR
Lama	VTVDVSTING	VAVACVGGCQ	AILDGTGTSVL	FGPSSDILKI	QKAIGATENR
Pig	FTVDSVTING	VVACVGGCQ	AILDGTGTSML	AGPSSDILNI	QMAIGATESQ
		301			350
Bos_bovis_chymosin_B	YGEFDIDCDN	LSYMPTVVFE	INGKMYPLTP	SAYTSQDQGF	CTSGFQSENH
C._bactrianus	YGEFDVNCGS	LRSMPPTVVFE	INGRDFPLAP	SAYTSKDQGF	CTSGFQGDNN
Camelus_dromedarius	YGEFDVNCGN	LRSMPPTVVFE	INGRDYPLSP	SAYTSKDQGF	CTSGFQGDNN
Lama	YGEFDVNCGN	LRSMPPTVVFE	INGRDYPLSP	SAYTSKDQGF	CTSGFQGDNN
Pig	YGEFDIDCGS	LSSMPTVVFE	ISGRMYPLPP	SAYTNQDQGF	CTSGFQGDNSK
		351		381	
Bos_bovis_chymosin_B	SQKWILGDVF	IREYYSVFDR	ANNLVGLAKA	I	
C._bactrianus	SELWILGDVF	IREYYSVFDR	ANNRVGLAKA	I	
Camelus_dromedarius	SELWILGDVF	IREYYSVFDR	ANNRVGLAKA	I	
Lama	SELWILGDVF	IREYYSVFDR	ANNRVGLAKA	I	
Pig	SQHWILGVVF	IQEYYSVFDR	ANNRVGLAKA	I	

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257964 entries***

CYB_CAMBA (Q34028)

Cytochrome b. {GENE: Name=MT-CYB; Synonyms=COB, CYTB, MTCYB} -
Camelus bactrianus (Bactrian camel)

HBA_CAMBA (P63105)

Hemoglobin subunit alpha (Hemoglobin alpha chain) (Alpha-globin). {GENE:
Name=HBA} - Camelus bactrianus (Bactrian camel)

HBB_CAMBA (P68230)

Hemoglobin subunit beta (Hemoglobin beta chain) (Beta-globin). {GENE: Name=HBB} - Camelus bactrianus (Bactrian camel)

IFNG_CAMBA (Q865W6)

Interferon gamma precursor (IFN-gamma). {GENE: Name=IFNG} - Camelus bactrianus (Bactrian camel)

IL13_CAMBA (Q865W5)

Interleukin-13 precursor (IL-13). {GENE: Name=IL13} - Camelus bactrianus (Bactrian camel)

IL2_CAMBA (Q2PE47)

Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF). {GENE: Name=IL2} - Camelus bactrianus (Bactrian camel)

IL6_CAMBA (Q865W7)

Interleukin-6 precursor (IL-6). {GENE: Name=IL6} - Camelus bactrianus (Bactrian camel)

RNAS1_CAMBA (P67929)

Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A). {GENE: Name=RNASE1; Synonyms=RNS1} - Camelus bactrianus (Bactrian camel)

TNFA_CAMBA (Q75N23)

Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor necrosis factor, membrane form; Tumor necrosis factor, soluble form]. {GENE: Name=TNF; Synonyms=TNFA, TNFSF2} - Camelus bactrianus (Bactrian camel)

Search in UniProtKB/TrEMBL: There are matches to 16 out of 3745801 entries

A1DZ82_CAMBA

Cytochrome b (Fragment) {GENE:Name=cytb} - Camelus bactrianus (Bactrian camel) [Mitochondrion]

A1ILB3_CAMBA

Transcription factor Tbx4 (Fragment) {GENE:Name=TBX4} - Camelus bactrianus (Bactrian camel)

A1ILB4_CAMBA

Transcription factor Tbx4 (Fragment) {GENE:Name=TBX4} - Camelus bactrianus (Bactrian camel)

Q2PE44_CAMBA

Interleukin-10 {GENE:Name=IL-10} - Camelus bactrianus (Bactrian camel)

Q2PE45_CAMBA

Interleukin-4 {GENE:Name=IL-4} - Camelus bactrianus (Bactrian camel)

Q2PE46_CAMBA

Interleukin-12p35 {GENE:Name=IL-12p35} - Camelus bactrianus (Bactrian camel)

Q3KRP3_CAMBA

Cytochrome c oxidase subunit II - Camelus bactrianus (Bactrian camel) [Mitochondrion]

Q540T9_CAMBA

Cytochrome b {GENE:Name=cytb} - Camelus bactrianus (Bactrian camel) [Mitochondrion]

Q68G96_CAMBA

Prion protein {GENE:Name=PrP} - Camelus bactrianus (Bactrian camel)

Q68G98_CAMBA

Prion protein {GENE:Name=PrP} - Camelus bactrianus (Bactrian camel)

Q68G99_CAMBA

Prion protein {GENE:Name=PrP} - Camelus bactrianus (Bactrian camel)

Q865W4_CAMBA

Interleukin 1 alpha (Fragment) {GENE:Name=IL-1 alpha} - Camelus bactrianus (Bactrian camel)

Q8HBR1_CAMBA

Cytochrome b {GENE:Name=cytb} - Camelus bactrianus (Bactrian camel)
[Mitochondrion]

Q8HFA7_CAMBA

Cytochrome b {GENE:Name=cytb} - Camelus bactrianus (Bactrian camel)
[Mitochondrion]

Q8HFA8_CAMBA

Cytochrome b {GENE:Name=cytb} - Camelus bactrianus (Bactrian camel)
[Mitochondrion]

Q9XS40_CAMBA

Ribonuclease X (Fragment) - Camelus bactrianus (Bactrian camel)

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CYB_LAMGL (Q34891)

Cytochrome b. {GENE: Name=MT-CYB; Synonyms=COB, CYTB, MTCYB} - Lama glama (Llama)

FIBA_LAMGL (P68218)

Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment). {GENE: Name=FGA} - Lama glama (Llama)

FIBB_LAMGL (P68122)

Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment). {GENE: Name=FGB}

- Lama glama (Llama)

HBA_LAMGL (P01973)
Hemoglobin subunit alpha (Hemoglobin alpha chain) (Alpha-globin). {GENE: Name=HBA} - Lama glama (Llama)

HBB_LAMGL (P68226)
Hemoglobin subunit beta (Hemoglobin beta chain) (Beta-globin). {GENE: Name=HBB} - Lama glama (Llama)

IFNG_CAMBA (Q865W6)
Interferon gamma precursor (IFN-gamma). {GENE: Name=IFNG} - Camelus bactrianus (Bactrian camel)

IFNG_LAMGL (Q865X1)
Interferon gamma precursor (IFN-gamma). {GENE: Name=IFNG} - Lama glama (Llama)

IL10_LAMGL (Q865X4)
Interleukin-10 precursor (IL-10) (Cytokine synthesis inhibitory factor) (CSIF). {GENE: Name=IL10} - Lama glama (Llama)

IL12A_LAMGL (Q865X0)
Interleukin-12 subunit alpha precursor (IL-12A) (IL-12 subunit p35) (Cytotoxic lymphocyte maturation factor 35 kDa subunit) (CLMF p35). {GENE: Name=IL12A} - Lama glama (Llama)

IL12B_LAMGL (Q865W9)
Interleukin-12 subunit beta precursor (IL-12B) (IL-12 subunit p40) (Cytotoxic lymphocyte maturation factor 40 kDa subunit) (CLMF p40). {GENE: Name=IL12B} - Lama glama (Llama)

IL13_CAMBA (Q865W5)
Interleukin-13 precursor (IL-13). {GENE: Name=IL13} - Camelus bactrianus (Bactrian camel)

IL13_LAMGL (Q865X3)
Interleukin-13 precursor (IL-13). {GENE: Name=IL13} - Lama glama (Llama)

IL1A_LAMGL (Q865X7)
Interleukin-1 alpha precursor (IL-1 alpha). {GENE: Name=IL1A} - Lama glama (Llama)

IL1B_LAMGL (Q865X8)
Interleukin-1 beta precursor (IL-1 beta). {GENE: Name=IL1B} - Lama glama (Llama)

IL2_LAMGL (Q865X2)
Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF). {GENE: Name=IL2} - Lama glama (Llama)

IL4_LAMGL (Q865X5)
Interleukin-4 precursor (IL-4) (B-cell stimulatory factor 1) (BSF-1) (Lymphocyte stimulatory factor 1). {GENE: Name=IL4} - Lama glama (Llama)

IL6_CAMBA (Q865W7)
Interleukin-6 precursor (IL-6). {GENE: Name=IL6} - Camelus bactrianus (Bactrian camel)

IL6_LAMGL (Q865X6)
Interleukin-6 precursor (IL-6). {GENE: Name=IL6} - Lama glama (Llama)

LCTN_LAMGL (P83315)
Lactophorin (Whey protein) (Fragment). - Lama glama (Llama)

NIR_PHOLA (Q51879)
Ferredoxin--nitrite reductase (EC 1.7.7.1). {GENE: Name=nirA; Synonyms=nir} - Phormidium lamosum

NRTB_PHOLA (Q51881)

Nitrate transport permease protein nrtB. {GENE: Name=nrtB} - Phormidium laminosum

TNFA_LAMGL (P59694)

Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor necrosis factor, membrane form; Tumor necrosis factor, soluble form]. {GENE: Name=TNF; Synonyms=TNFA, TNFSF2} - Lama glama (Llama)

TSHB_LAMGL (P79357)

Thyrotropin subunit beta precursor (Thyroid-stimulating hormone subunit beta) (TSH-beta) (TSH-B) (Thyrotropin beta chain). {GENE: Name=TSHB} - Lama glama (Llama)

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A0SMH6_LAMGL

Cytochrome c oxidase subunit III (Fragment) {GENE:Name=COXIII} - Lama glama (Llama) [Mitochondrion]

O97643_LAMGL

Fibrinogen A-alpha chain (Fragment) - Lama glama (Llama)

O97696_LAMGL

Prion protein (Fragment) {GENE:Name=PrP} - Lama glama (Llama)

P79356_LAMGU

Sex-determining protein (Fragment) {GENE:Name=Sry} - Lama guanicoe (Guanaco)

Q3KRP9_LAMGL

Cytochrome c oxidase subunit II - Lama glama (Llama) [Mitochondrion]

Q4F895_RHOER

Aldehyde dehydrogenase {GENE:Name=aldhR} - Rhodococcus erythropolis

Q4ZGZ7_PHOLA

NrtD {GENE:Name=nrtD} - Phormidium laminosum 'OH-1-p Cl 1'

Q4ZGZ8_PHOLA

NrtC {GENE:Name=nrtC} - Phormidium laminosum 'OH-1-p Cl 1'

Q51880_PHOLA

Probable periplasmic protein {GENE:Name=nrtA-Phl} - Phormidium laminosum

Q51882_PHOLA

ATP binding protein {GENE:Name=nrtC-Phl} - Phormidium laminosum

Q7YR06_LAMGL

Apolipoprotein B (Fragment) - Lama glama (Llama)

Q865W4_CAMBA

Interleukin 1 alpha (Fragment) {GENE:Name=IL-1 alpha} - Camelus bactrianus (Bactrian camel)

Q865W8_LAMGL

Beta actin (Fragment) - Lama glama (Llama)

Q8GC77_ERWCH

PagP protein {GENE:Name=pagP} - Erwinia chrysanthemi

Q8GC78_ERWCH

PhoQ protein {GENE:Name=phoQ} - Erwinia chrysanthemi

Q8GC79_ERWCH
PhoP protein {GENE:Name=phoP} - *Erwinia chrysanthemi*

Q8GCZ3_PHOLA
Global nitrogen control protein (Fragment) {GENE:Name=ntcA} - *Phormidium laminosum*

Q8W8W9_LAMVI
Cytochrome b (Fragment) - *Lama vicugna* (*Vicugna*) (*Vicugna vicugna*) [Mitochondrion]

Q8W8X0_LAMPA
Cytochrome b (Fragment) - *Lama guanicoe pacos* (*Alpaca*) (*Lama pacos*) [Mitochondrion]

Q8W8X1_LAMGU
Cytochrome b (Fragment) - *Lama guanicoe* (*Guanaco*) [Mitochondrion]

Q8W8X2_LAMGL
Cytochrome b (Fragment) - *Lama glama* (*Llama*) [Mitochondrion]

Q8WD32_LAMPA
Cytochrome b (Fragment) - *Lama guanicoe pacos* (*Alpaca*) (*Lama pacos*) [Mitochondrion]

Q8WD33_LAMPA
Cytochrome b (Fragment) - *Lama guanicoe pacos* (*Alpaca*) (*Lama pacos*) [Mitochondrion]

Q8WD34_LAMGL
Cytochrome b (Fragment) - *Lama glama* (*Llama*) [Mitochondrion]

Q8WD35_LAMGU
Cytochrome b (Fragment) - *Lama guanicoe* (*Guanaco*) [Mitochondrion]

Q93KB5_ERWCH
Putative antibiotic biosynthesis protein {GENE:Name=pab} - *Erwinia chrysanthemi*

Q93KB6_ERWCH
Putative ABC transporter {GENE:Name=ybit} - *Erwinia chrysanthemi*

Q9BDS1_LAMGL
Recombination activating protein 2 (Fragment) {GENE:Name=rag2} - *Lama glama* (*Llama*)

Q9BDS2_LAMGL
Recombination activating protein 1 {GENE:Name=rag1} - *Lama glama* (*Llama*)

Q9BDV2_LAMGL
BRCA1 (Fragment) - *Lama glama* (*Llama*)

Q9BEJ5_LAMGL
Zinc finger protein ZFX (Fragment) {GENE:Name=ZFX} - *Lama glama* (*Llama*)

Q9BEN3_LAMGL
Tyrosinase (Fragment) {GENE:Name=TYR} - *Lama glama* (*Llama*)

Q9BES5_LAMGL
Recombination activating protein 2 (Fragment) {GENE:Name=RAG2} - *Lama glama* (*Llama*)

Q9BEW8_LAMGL
Recombination activating protein 1 (Fragment) {GENE:Name=RAG1} - *Lama glama* (*Llama*)

Q9BF09_LAMGL
Prepronociceptin (Fragment) {GENE:Name=PNOC} - *Lama glama* (*Llama*)

Q9BFD4_LAMGL
Cannabinoid receptor 1 (Fragment) {GENE:Name=CNR1} - *Lama glama* (*Llama*)

Q9BFI2_LAMGL

Brain-derived neurotrophic factor (Fragment) {GENE:Name=BDNF} - Lama glama (Llama)

Q9BFM8_LAMGL

ATP7A (Fragment) {GENE:Name=ATP7A} - Lama glama (Llama)

Q9BFS6_LAMGL

Amyloid beta protein (Fragment) {GENE:Name=APP} - Lama glama (Llama)

Q9BFX3_LAMGL

Beta-2 adrenergic receptor (Fragment) {GENE:Name=ADRB2} - Lama glama (Llama)

Q9BG17_LAMGL

Adenosine A3 receptor (Fragment) {GENE:Name=ADORA3} - Lama glama (Llama)

Q9XSA4_LAMGL

Von Willebrand factor (Fragment) {GENE:Name=vWF} - Lama glama (Llama)

Q9XSA5_LAMGL

Interphotoreceptor retinoid binding protein (Fragment) {GENE:Name=IRBP} - Lama glama (Llama)

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CYB_LAMVI (Q36227)

Cytochrome b. {GENE: Name=MT-CYB; Synonyms=COB, CYTB, MTCYB} - Lama vicugna (Vicugna) (Vicugna vicugna)

FIBA_LAMVI (P68219)

Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment). {GENE: Name=FGA} - Lama vicugna (Vicugna) (Vicugna vicugna)

FIBB_LAMVI (P68124)

Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment). {GENE: Name=FGB}

- Lama vicugna (Vicugna) (Vicugna vicugna)
HBA_LAMPA (**P67816**)
Hemoglobin subunit alpha (Hemoglobin alpha chain) (Alpha-globin). {GENE:
Name=HBA} - Lama guanicoe pacos (Alpaca) (Lama pacos)
HBA_LAMVI (**P07425**)
Hemoglobin subunit alpha (Hemoglobin alpha chain) (Alpha-globin). {GENE:
Name=HBA} - Lama vicugna (Vicugna) (Vicugna vicugna)
HBB_LAMVI (**P68227**)
Hemoglobin subunit beta (Hemoglobin beta chain) (Beta-globin). {GENE:
Name=HBB} - Lama vicugna (Vicugna) (Vicugna vicugna)

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A0SMH8_LAMVI
Cytochrome c oxidase subunit III (Fragment) {GENE:Name=COXIII} - Lama vicugna
(Vicugna) (Vicugna vicugna) [Mitochondrion]
Q206M5_LAMVI
Urokinase-type plasminogen activator (Fragment) - Lama vicugna (Vicugna)
(Vicugna vicugna)
Q3KRP6_LAMVI
Cytochrome c oxidase subunit II - Lama vicugna (Vicugna) (Vicugna vicugna)
[Mitochondrion]
Q5GH07_LAMVI
Cytochrome b {GENE:Name=cytb} - Vicugna vicugna mensalis [Mitochondrion]
Q8W8W9_LAMVI
Cytochrome b (Fragment) - Lama vicugna (Vicugna) (Vicugna vicugna)
[Mitochondrion]

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257964 entries***

ACTB_CAMDR (P84336)

Actin, cytoplasmic 1 (Beta-actin). {GENE: Name=ACTB} - Camelus dromedarius
(Dromedary) (Arabian camel)

CASA1_CAMDR (O97943)

Alpha-S1-casein precursor. {GENE: Name=CSN1S1} - Camelus dromedarius
(Dromedary) (Arabian camel)

CASA2_CAMDR (O97944)

Alpha-S2-casein precursor. {GENE: Name=CSN1S2} - Camelus dromedarius (Dromedary) (Arabian camel)

CASB_CAMDR (Q9TVD0)

Beta-casein precursor. {GENE: Name=CSN2} - Camelus dromedarius (Dromedary) (Arabian camel)

CASK_CAMDR (P79139)

Kappa-casein precursor. {GENE: Name=CSN3; Synonyms=CSN10, CSNK} - Camelus dromedarius (Dromedary) (Arabian camel)

CFDP1_CAMDR (Q4ADK7)

Craniofacial development protein 1 (Bucentaur). {GENE: Name=CFDP1; Synonyms=BCNT} - Camelus dromedarius (Dromedary) (Arabian camel)

COLI_CAMDR (P01203)

Beta-endorphin [Contains: Met-enkephalin]. - Camelus dromedarius (Dromedary) (Arabian camel)

CRYAA_CAMDR (P02472)

Alpha crystallin A chain [Contains: Alpha crystallin A chain, short form]. {GENE: Name=CRYAA} - Camelus dromedarius (Dromedary) (Arabian camel)

CYB_CAMDR (P24952)

Cytochrome b. {GENE: Name=MT-CYB; Synonyms=COB, CYTB, MTCYB} - Camelus dromedarius (Dromedary) (Arabian camel)

CYC_CAMDR (P68099)

Cytochrome c. {GENE: Name=CYCS; Synonyms=CYC} - Camelus dromedarius (Dromedary) (Arabian camel)

FIBA_CAMDR (P14444)

Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment). {GENE: Name=FGA} - Camelus dromedarius (Dromedary) (Arabian camel)

FIBB_CAMDR (P68123)

Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment). {GENE: Name=FGB} - Camelus dromedarius (Dromedary) (Arabian camel)

GLUC_CAMDR (P68273)

Glucagon. {GENE: Name=GCG} - Camelus dromedarius (Dromedary) (Arabian camel)

HBA_CAMDR (P63106)

Hemoglobin subunit alpha (Hemoglobin alpha chain) (Alpha-globin). {GENE: Name=HBA} - Camelus dromedarius (Dromedary) (Arabian camel)

HBB_CAMDR (P68231)

Hemoglobin subunit beta (Hemoglobin beta chain) (Beta-globin). {GENE: Name=HBB} - Camelus dromedarius (Dromedary) (Arabian camel)

INS_CAMDR (P01320)

Insulin [Contains: Insulin B chain; Insulin A chain]. {GENE: Name=INS} - Camelus dromedarius (Dromedary) (Arabian camel)

LALBA_CAMDR (P00710)

Alpha-lactalbumin (Lactose synthase B protein). {GENE: Name=LALBA} - Camelus dromedarius (Dromedary) (Arabian camel)

LCTN_CAMDR (P15522)

Lactophorin precursor (Whey protein) (Proteose-peptone component 3) (PP3). - Camelus dromedarius (Dromedary) (Arabian camel)

LCTN_LAMGL (P83315)

Lactophorin (Whey protein) (Fragment). - Lama glama (Llama)

LYSC_CAMDR (P37712)

Lysozyme C (EC 3.2.1.17) (1,4-beta-N-acetylmuramidase). {GENE: Name=LYZ} -
Camelus dromedarius (Dromedary) (Arabian camel)

MLA_CAMDR (P61281)

Melanotropin alpha (Alpha-MSH). - Camelus dromedarius (Dromedary) (Arabian camel)

PGRP_CAMDR (Q9GK12)

Peptidoglycan recognition protein precursor (Peptidoglycan recognition protein short) (PGRP-S). {GENE: Name=PGLYRP1; Synonyms=PGLYRP, PGRP} -
Camelus dromedarius (Dromedary) (Arabian camel)

PRIO_CAMDR (P79141)

Major prion protein precursor (PrP) (CD230 antigen). {GENE: Name=PRNP; Synonyms=PRP} - Camelus dromedarius (Dromedary) (Arabian camel)

PRL_CAMDR (P22393)

Prolactin (PRL). {GENE: Name=PRL} - Camelus dromedarius (Dromedary) (Arabian camel)

RNAS1_CAMDR (P67928)

Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A). {GENE: Name=RNASE1; Synonyms=RNS1} - Camelus dromedarius (Dromedary) (Arabian camel)

SOMA_CAMDR (Q7YRR6)

Somatotropin precursor (Growth hormone). {GENE: Name=GH1; Synonyms=GH} -
Camelus dromedarius (Dromedary) (Arabian camel)

TRFL_CAMDR (Q9TUM0)

Lactotransferrin precursor (EC 3.4.21.-) (Lactoferrin). {GENE: Name=LTF} -
Camelus dromedarius (Dromedary) (Arabian camel)

UBIQ_CAMDR (Q865C5)

Ubiquitin. - Camelus dromedarius (Dromedary) (Arabian camel)

WAP_CAMDR (P09837)

Whey acidic protein (WAP). {GENE: Name=WAP} - Camelus dromedarius (Dromedary) (Arabian camel)

Search in UniProtKB/TrEMBL: There are matches to 26 out of 3745801 entries

O02677_CAMDR

Gamma fibrinogen (Fragment) - Camelus dromedarius (Dromedary) (Arabian camel)

Q1RP86_CAMDR

Tyrosine kinase receptor 2 (Fragment) {GENE:Name=tie2} - Camelus dromedarius (Dromedary) (Arabian camel)

Q1RP87_CAMDR

Vascular endothelial growth factor isoform 121 (Fragment) {GENE:Name=vegf} -
Camelus dromedarius (Dromedary) (Arabian camel)

Q1RP88_CAMDR

Progesterone receptor (Fragment) {GENE:Name=pr} - Camelus dromedarius (Dromedary) (Arabian camel)

Q1RP89_CAMDR

Estrogen receptor alpha (Fragment) {GENE:Name=er alpha} - Camelus

dromedarius (Dromedary) (Arabian camel)
Q28229_CAMDR
B-casein (Fragment) - Camelus dromedarius (Dromedary) (Arabian camel)
Q28231_CAMDR
Estrogen receptor (Fragment) {GENE:Name=ER} - Camelus dromedarius (Dromedary) (Arabian camel)
Q2KN22_CAMDR
Neonatal Fc receptor alpha-chain {GENE:Name=FCGRT} - Camelus dromedarius (Dromedary) (Arabian camel)
Q3KRP2_CAMDR
Cytochrome c oxidase subunit II - Camelus dromedarius (Dromedary) (Arabian camel) [Mitochondrion]
Q6L7Z3_CAMDR
B-type natriuretic peptide precursor {GENE:Name=BNP} - Camelus dromedarius (Dromedary) (Arabian camel)
Q6L7Z4_CAMDR
Atrial natriuretic peptide precursor {GENE:Name=ANP} - Camelus dromedarius (Dromedary) (Arabian camel)
Q864E3_CAMDR
Recombination activating protein 1 (Fragment) {GENE:Name=RAG-1} - Camelus dromedarius (Dromedary) (Arabian camel)
Q864U9_CAMDR
Leptin receptor long isoform (Fragment) - Camelus dromedarius (Dromedary) (Arabian camel)
Q864V0_CAMDR
Leptin receptor short isoform (Fragment) - Camelus dromedarius (Dromedary) (Arabian camel)
Q864V1_CAMDR
Leptin (Fragment) - Camelus dromedarius (Dromedary) (Arabian camel)
Q8HB83_CAMDR
Cytochrome b {GENE:Name=cytb} - Camelus dromedarius (Dromedary) (Arabian camel) [Mitochondrion]
Q8HBG5_CAMDR
Cytochrome b {GENE:Name=cytb} - Camelus dromedarius (Dromedary) (Arabian camel) [Mitochondrion]
Q8HZ65_CAMDR
Presenilin-1 (Fragment) - Camelus dromedarius (Dromedary) (Arabian camel)
Q8WMP6_CAMDR
Alpha-lactalbumin (Fragment) {GENE:Name=lalba} - Camelus dromedarius (Dromedary) (Arabian camel)
Q9GJW6_CAMDR
Peroxidase precursor (EC 1.11.1.7) {GENE:Name=lactoperoxidase} - Camelus dromedarius (Dromedary) (Arabian camel)
Q9GK10_CAMDR
Pepsin A precursor (EC 3.4.23.1) {GENE:Name=pepsin} - Camelus dromedarius (Dromedary) (Arabian camel)
Q9GK11_CAMDR
Chymosin precursor (EC 3.4.23.4) {GENE:Name=chymosin} - Camelus dromedarius (Dromedary) (Arabian camel)
Q9N0T9_CAMDR

Preprorelaxin - *Camelus dromedarius* (Dromedary) (Arabian camel)
Q9TS81_CAMDR
Glycerol ester HYDROLAS (EC 3.1.1.3) (Fragments) - *Camelus dromedarius*
(Dromedary) (Arabian camel)
Q9TV02_CAMDR
Prion protein (Fragment) {GENE:Name=PrP} - *Camelus dromedarius* (Dromedary)
(Arabian camel)
Q9TVB7_CAMDR
Pancreatic ribonuclease (EC 3.1.27.5) (Fragment) - *Camelus dromedarius*
(Dromedary) (Arabian camel)

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If your question is not covered, please contact <helpdesk@expasy.org>.

NCBI BLAST program reference [PMID:9254694]:
Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

Query: 379 AA
Date run: 2007-02-15 21:49:25 UTC+0100 on blast01.vital-it.ch
Program: NCBI BLASTP 2.2.15 [Oct-15-2006]
Database: UniProtKB Mammalia
240,475 sequences; 91,865,493 total letters
UniProt Knowledgebase Release 9.6 consists of:
UniProtKB/Swiss-Prot Release 51.6 of 06-Feb-2007: 257964 entries
UniProtKB/TrEMBL Release 34.6 of 06-Feb-2007: 3745801 entries

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List of potentially matching sequences


Send selected sequences to ☐ Include query sequence

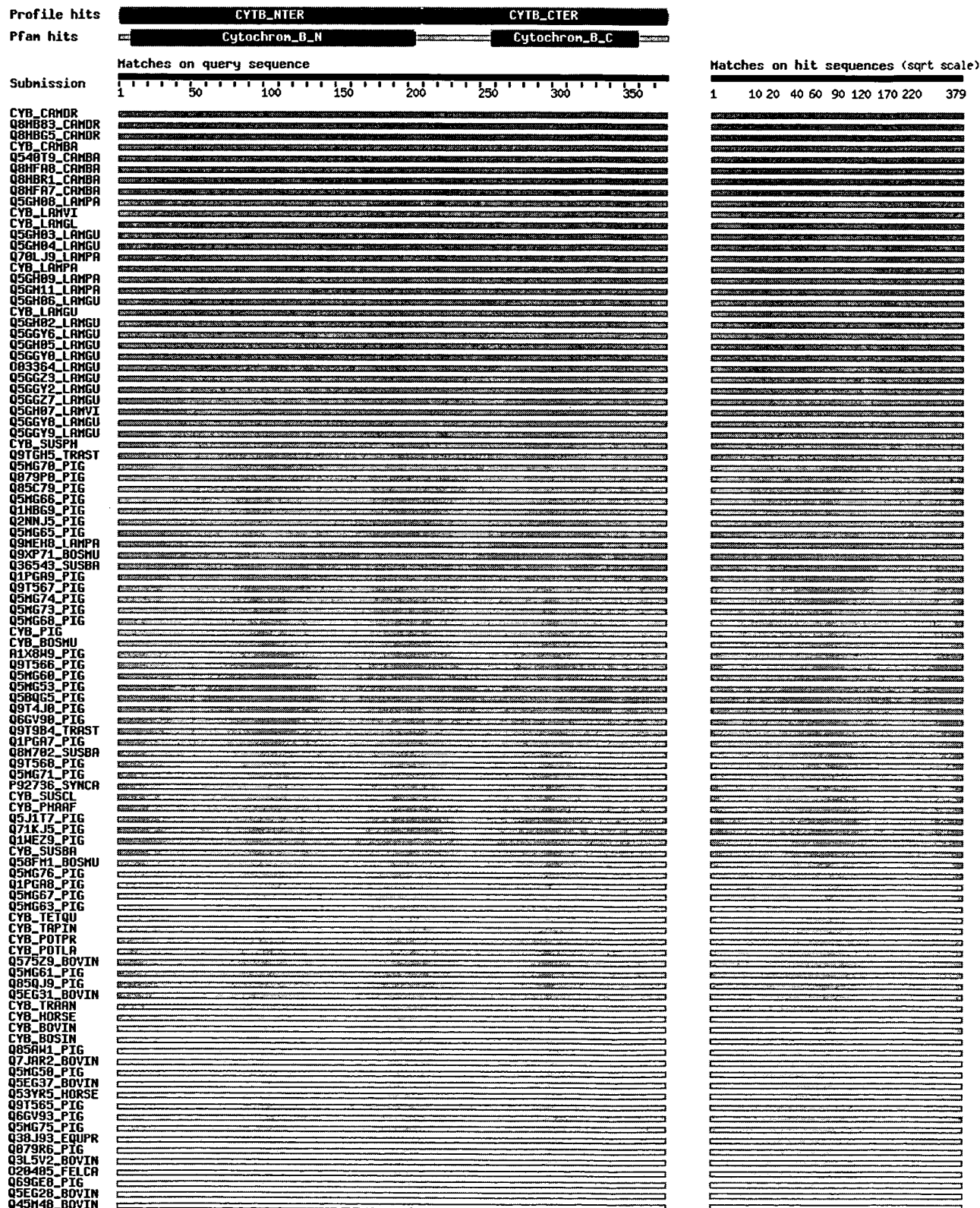
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<input type="checkbox"/> tr Q8HB83	_CAMDR Cytochrome b [cytb] [Camelus dromedarius (Dromed...	775 0.0
<input type="checkbox"/> tr Q8HBG5	_CAMDR Cytochrome b [cytb] [Camelus dromedarius (Dromed...	773 0.0
<input type="checkbox"/> sp Q34028	CYB_CAMBA Cytochrome b [MT-CYB] [Camelus bactrianus (B...	763 0.0
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<input type="checkbox"/> tr Q8HBR1	_CAMBA Cytochrome b [cytb] [Camelus bactrianus (Bactria...	754 0.0
<input type="checkbox"/> tr Q8HFA7	_CAMBA Cytochrome b [cytb] [Camelus bactrianus (Bactria...	753 0.0
<input type="checkbox"/> tr Q5GH08	_LAMPA Cytochrome b [cytb] [Lama glama argentina]	747 0.0
<input type="checkbox"/> sp Q36227	CYB_LAMVI Cytochrome b [MT-CYB] [Lama vicugna (Vicugna...	745 0.0
<input type="checkbox"/> sp Q34891	CYB_LAMGL Cytochrome b [MT-CYB] [Lama glama (Llama)]	745 0.0
<input type="checkbox"/> tr Q5GH03	_LAMGU Cytochrome b [cytb] [Lama guanicoe huanacus]	745 0.0
<input type="checkbox"/> tr Q5GH04	_LAMGU Cytochrome b [cytb] [Lama guanicoe cacsilensis]	745 0.0
<input type="checkbox"/> tr Q70LJ9	_LAMPA Cytochrome b [cytb] [Lama guanicoe pacos (Alpaca...	745 0.0
<input type="checkbox"/> sp Q34916	CYB_LAMPA Cytochrome b [MT-CYB] [Lama guanicoe pacos (...]	744 0.0
<input type="checkbox"/> tr Q5GH09	_LAMPA Cytochrome b [cytb] [Lama glama chaku]	744 0.0
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<input type="checkbox"/> tr Q5GH06	_LAMGU Cytochrome b [cytb] [Lama guanicoe cacsilensis]	743 0.0
<input type="checkbox"/> sp Q34890	CYB_LAMGU Cytochrome b [MT-CYB] [Lama guanicoe (Guanaco)]	742 0.0
<input type="checkbox"/> tr Q5GH02	_LAMGU Cytochrome b [cytb] [Lama guanicoe huanacus]	742 0.0
<input type="checkbox"/> tr Q5GGY6	_LAMGU Cytochrome b [cytb] [Lama guanicoe guanicoe]	742 0.0
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<input type="checkbox"/> tr O03364	_LAMGU Cytochrome b [Lama guanicoe (Guanaco)]	741 0.0
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<input type="checkbox"/> tr Q5GH07	_LAMVI Cytochrome b [cytb] [Vicugna vicugna mensalis]	739 0.0
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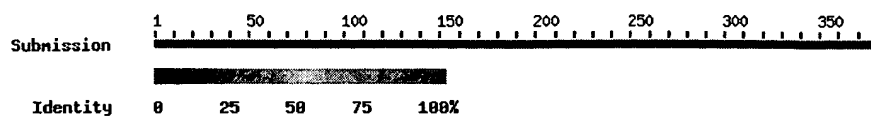
<input type="checkbox"/>	tr Q9TGH5	_TRAST Cytochrome b [cytb]	[Tragelaphus strepsiceros (G...]	723	0.0
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<input type="checkbox"/>	tr Q5MG65	_PIG Cytochrome b [CYTB]	[Sus scrofa coreanus]	721	0.0
<input type="checkbox"/>	tr Q9MEH8	_LAMPA Cytochrome b [Cyt b]	[Lama guanicoe pacos (Alpac...]	721	0.0
<input type="checkbox"/>	tr Q9XP71	_BOSMU Cytochrome b [cytb]	[Bos mutus grunniens (Wild y...]	721	0.0
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<input type="checkbox"/>	tr Q1PGA9	_PIG Cytochrome b [Sus scrofa (Pig)]		721	0.0
<input type="checkbox"/>	tr Q9T567	_PIG Cytochrome b [cytb]	[Sus scrofa (Pig)]	720	0.0
<input type="checkbox"/>	tr Q5MG74	_PIG Cytochrome b [CYTB]	[Sus scrofa coreanus]	720	0.0
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<input type="checkbox"/>	tr A1X8W9	_PIG Cytochrome b [Sus scrofa (Pig)]		720	0.0
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<input type="checkbox"/>	tr Q9T9B4	_TRAST Cytochrome b [cytb]	[Tragelaphus strepsiceros (G...]	719	0.0
<input type="checkbox"/>	tr Q1PGA7	_PIG Cytochrome b [Sus scrofa (Pig)]		719	0.0
<input type="checkbox"/>	tr Q8M702	_SUSBA Cytochrome b [cyt-B]	[Sus barbatus (Bearded pig)]	719	0.0
<input type="checkbox"/>	tr Q9T568	_PIG Cytochrome b [cytb]	[Sus scrofa (Pig)]	719	0.0
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<input type="checkbox"/>	tr P92736	_SYNCA Cytochrome b [Syncherus caffer (Cape buffalo)]		719	0.0
<input type="checkbox"/>	sp Q5J1T5	CYB_SUSCL Cytochrome b [MT-CYB]	[Sus celebensis (Celeb...]	719	0.0
<input type="checkbox"/>	sp Q8M706	CYB_PHAAP Cytochrome b [MT-CYB]	[Phacochoerus africanu...]	719	0.0
<input type="checkbox"/>	tr Q5J1T7	_PIG Cytochrome b [cytb]	[Sus scrofa (Pig)]	719	0.0
<input type="checkbox"/>	tr Q71KJ5	_PIG Cytochrome b [CYTB]	[Sus scrofa (Pig)]	719	0.0
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<input type="checkbox"/>	tr Q58FM1	_BOSMU Cytochrome b [cytb]	[Bos grunniens mutus]	718	0.0
<input type="checkbox"/>	tr Q5MG76	_PIG Cytochrome b [CYTB]	[Sus scrofa coreanus]	718	0.0
<input type="checkbox"/>	tr Q1PGA8	_PIG Cytochrome b [Sus scrofa (Pig)]		718	0.0
<input type="checkbox"/>	tr Q5MG67	_PIG Cytochrome b [CYTB]	[Sus scrofa coreanus]	718	0.0
<input type="checkbox"/>	tr Q5MG63	_PIG Cytochrome b [CYTB]	[Sus scrofa (Pig)]	718	0.0
<input type="checkbox"/>	sp Q9T9C0	CYB_TETQU Cytochrome b [MT-CYB]	[Tetracerus quadricorn...]	717	0.0
<input type="checkbox"/>	sp Q9T7T9	CYB_TAPIN Cytochrome b [MT-CYB]	[Tapirus indicus (Asia...]	717	0.0
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<input type="checkbox"/>	sp Q5J1T3	CYB_POTLA Cytochrome b [MT-CYB]	[Potamochoerus larvatu...]	717	0.0
<input type="checkbox"/>	tr Q575Z9	_BOVIN Cytochrome b [Cytb]	[Bos taurus (Bovine)]	717	0.0
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<input type="checkbox"/>	tr Q85QJ9	_PIG Cytochrome b [cytb]	[Sus scrofa (Pig)]	717	0.0
<input type="checkbox"/>	tr Q5EG31	_BOVIN Cytochrome b [Bos taurus (Bovine)]		717	0.0
<input type="checkbox"/>	sp Q9TG16	CYB_TRAAN Cytochrome b [MT-CYB]	[Tragelaphus angasii (...]	717	0.0
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<input type="checkbox"/>	tr Q5MG50	_PIG Cytochrome b [CYTB]	[Sus scrofa (Pig)]	717	0.0
<input type="checkbox"/>	tr Q5EG37	_BOVIN Cytochrome b [Bos taurus (Bovine)]		717	0.0
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<input type="checkbox"/>	tr Q9T565	_PIG Cytochrome b [cytb]	[Sus scrofa (Pig)]	717	0.0
<input type="checkbox"/>	tr Q6GV93	_PIG Cytochrome b [CYTB]	[Sus scrofa (Pig)]	717	0.0
<input type="checkbox"/>	tr Q5MG75	_PIG Cytochrome b [CYTB]	[Sus scrofa coreanus]	717	0.0
<input type="checkbox"/>	tr Q38J93	_EQUPR Cytochrome b [CYTB]	[Equus caballus przewalskii ...]	717	0.0
<input type="checkbox"/>	tr Q079R6	_PIG Cytochrome b [CYTB]	[Sus scrofa (Pig)]	717	0.0
<input type="checkbox"/>	tr Q3L5V2	_BOVIN Cytochrome b [CYTB]	[Bos taurus (Bovine)]	717	0.0
<input type="checkbox"/>	tr O20405	_FELCA Cytochrome b [Felis silvestris catus (Cat)]		717	0.0

☐ tr Q69GE8 _PIG Cytochrome b [CYTB] [Sus scrofa (Pig)] 717 0.0
☐ tr Q5EG28 _BOVIN Cytochrome b [CYTB] [Bos taurus (Bovine)] 717 0.0
☐ tr Q45M48 _BOVIN Cytochrome b [CYTB] [Bos taurus (Bovine)] 717 0.0

Graphical overview of the alignments

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Alignments

sp P24952 Cytochrome b [MT-CYB] [Camelus dromedarius (Dromedary) (Arabian 379 AA
CYB_CAMDR camel)] align

Score = 776 bits (2004), Expect = 0.0
Identities = 379/379 (100%), Positives = 379/379 (100%)

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MTNIRKSHPLLKIMNDAFIDLPA PNSSW NFGSLLGVCLIMQILTGLFLAMHYTSDTT
Sbjct: 1 MTNIRKSHPLLKIMNDAFIDLPA PNSSW NFGSLLGVCLIMQILTGLFLAMHYTSDTT 60

Query: 61 TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL
Sbjct: 61 TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWINGGFSVDKATLTRFFA 180
FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWINGGFSVDKATLTRFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWINGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLMLLALL 240
FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLMLLALL
Sbjct: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLMLLALL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI
Sbjct: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQVPEPPFIMIGQVASILYFS 360
LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQVPEPPFIMIGQVASILYFS
Sbjct: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQVPEPPFIMIGQVASILYFS 360

Query: 361 LILILMPVAGIENRILKW 379
LILILMPVAGIENRILKW
Sbjct: 361 LILILMPVAGIENRILKW 379

tr Q8HB83 Cytochrome b [cytb] [Camelus dromedarius (Dromedary) (Arabian 379 AA
Q8HB83_CAMDR camel)] align

Score = 775 bits (2000), Expect = 0.0
Identities = 378/379 (99%), Positives = 379/379 (100%)

Query: 1 MTNIRKSHPLLKIMNDAFIDLPA PNSSW NFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
MTNIRKSHPLLKIMNDAFIDLPA PNSSW NFGSLLGVCLIMQILTGLFLAMHYTSDTT
Sbjct: 1 MTNIRKSHPLLKIMNDAFIDLPA PNSSW NFGSLLGVCLIMQILTGLFLAMHYTSDTT 60

Query: 61 TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL
Sbjct: 61 TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWINGGFSVDKATLTRFFA 180
FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWINGGFSVDKATLTRFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWINGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLMLLALL 240
FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLMLLALL
Sbjct: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLMLLALL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI
Sbjct: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQVPEPPFIMIGQVASILYFS 360
LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQVPEPPFIMIGQVASILYFS
Sbjct: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQVPEPPFIMIGQVASILYFS 360

Query: 361 LILILMPVAGIENRILKW 379
LILILMPVAGIENRILKW
Sbjct: 361 LILILMPVAGIENRILKW 379

tr Q8HBG5 Cytochrome b [cytb] [Camelus dromedarius (Dromedary) (Arabian camel)] 379 AA
Q8HBG5_CAMDR camel]] align

Score = 773 bits (1995), Expect = 0.0
Identities = 377/379 (99%), Positives = 378/379 (99%)

Query: 1 MTNIRKSHPLLKIMNDAFIDLPAISNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
MTNIRKSHPLLKIMNDAFIDLPAISNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT
Sbjct: 1 MTNIRKSHPLLKIMNDAFIDLPAISNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60

Query: 61 TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYGYSTFSETWNVGMVLL 120
TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYGYSTFSETWNVG+VLL
Sbjct: 61 TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYGYSTFSETWNVGIVLL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180
FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISDDMDKIPFHPYYTIKDILGALLMLLALL 240
FHFILPFIITALVAVHLLFLHETGSNNPTGI SDMDKIPFHPYYTIKDILGALLMLLALL
Sbjct: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGIPSDMDKIPFHPYYTIKDILGALLMLLALL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLAIVLSILI 300
ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLAIVLSILI
Sbjct: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLAIVLSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQVPEPPFIMIGQVASILYFS 360
LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQVPEPPFIMIGQVASILYFS
Sbjct: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQVPEPPFIMIGQVASILYFS 360

Query: 361 LILILMPVAGIENRILKW 379
LILILMPVAGIENRILKW
Sbjct: 361 LILILMPVAGIENRILKW 379

sp Q34028 Cytochrome b [MT-CYB] [Camelus bactrianus (Bactrian camel)] 379 AA
CYB_CAMBA align

Score = 763 bits (1970), Expect = 0.0
Identities = 371/379 (97%), Positives = 374/379 (98%)

Query: 1 MTNIRKSHPLLKIMNDAFIDLPAISNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
MTNIRKSHPLLKIMNDAFIDLPAISNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT
Sbjct: 1 MTNIRKSHPLLKIMNDAFIDLPAISNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60

Query: 61 TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYGYSTFSETWNVGMVLL 120
TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYGYSTF ETWNVG++LL
Sbjct: 61 TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYGYSTFLETWNVGIILL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180
FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISDDMDKIPFHPYYTIKDILGALLMLLALL 240
FHFILPFIITALVAVHLLFLHETGSNNPTGISDDMDKIPFHPYYTIKDILGALLML LL
Sbjct: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISDDMDKIPFHPYYTIKDILGALLMLLILL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLAIVLSILI 300
ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLAIVLSILI
Sbjct: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLAIVLSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQVPEPPFIMIGQVASILYFS 360
LA IP LHTSKQSRM FRPISQCLFWVLVADLLTLTWIGGQVPEPPFIMIGQVASILYFS
Sbjct: 301 LALIPMLHTSKQRSMMFRPISQCLFWVLVADLLTLTWIGGQVPEPPFIMIGQVASILYFS 360

Query: 361 LILILMPVAGIENRILKW 379
LILILMPVAGIENRILKW
Sbjct: 361 LILILMPVAGIENRILKW 379

tr Q540T9 Cytochrome b [cytb] [Camelus bactrianus (Bactrian camel)] 379 AA
Q540T9_CAMBA align

Score = 763 bits (1970), Expect = 0.0
Identities = 371/379 (97%), Positives = 374/379 (98%)

Query: 1 MTNIRKSHPLLKIMNDAFIDLPAISNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
MTNIRKSHPLLKIMNDAFIDLPAISNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT
Sbjct: 1 MTNIRKSHPLLKIMNDAFIDLPAISNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60

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Query: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
          TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTF ETWNVG++LL
Sbjct: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFLETWNVGIILL 120

Query: 121 FTVMATAFMGVYLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180
          FTVMATAFMGVYLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA
Sbjct: 121 FTVMATAFMGVYLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLMLLALL 240
          FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLMLL LL
Sbjct: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLMLLILL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
          ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLAL+LSILI
Sbjct: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALILSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQVPEPPFIMIGQVASILYFS 360
          LA IP LHTSKQSRM FRPISQCLFWVLVADLLTLTWIGGQVPEPPFIMIGQVASILYFS
Sbjct: 301 LALIPMLHTSKQRSMMFRPISQCLFWVLVADLLTLTWIGGQVPEPPFIMIGQVASILYFS 360

Query: 361 LILILMPVAGIENRILKW 379
          LILILMPVAGIENRILKW
Sbjct: 361 LILILMPVAGIENRILKW 379

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tr Q8HFA8      Cytochrome b [cytb] [Camelus bactrianus (Bactrian camel)] 379 AA
Q8HFA8_CAMBA align

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Score = 759 bits (1959), Expect = 0.0
Identities = 369/379 (97%), Positives = 372/379 (98%)

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Query: 1  MTNIRKSHPLLKIMNDAFIDLPAISNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
          MTNIRKSHPLLKIMNDAFIDLPAISNISSWWNFGSLLGVCLI QILTGLFLAMHYTSDTT
Sbjct: 1  MTNIRKSHPLLKIMNDAFIDLPAISNISSWWNFGSLLGVCLITQILTGLFLAMHYTSDTT 60

Query: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
          TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTF ETWNVG++LL
Sbjct: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFLETWNVGIILL 120

Query: 121 FTVMATAFMGVYLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180
          FTVMATAFMGVYLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA
Sbjct: 121 FTVMATAFMGVYLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLMLLALL 240
          FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLMLL LL
Sbjct: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLMLLILL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
          ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLAL+LSILI
Sbjct: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALILSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQVPEPPFIMIGQVASILYFS 360
          LA IP LHTSKQSRM FRPISQCLFWVLVADLL TLTWIGGQVPEPPFIMIGQVASILYFS
Sbjct: 301 LALIPMLHTSKQRSMMFRPISQCLFWVLVADLLALTWIGGQVPEPPFIMIGQVASILYFS 360

Query: 361 LILILMPVAGIENRILKW 379
          LILILMPVAGIENRILKW
Sbjct: 361 LILILMPVAGIENRILKW 379

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tr Q8HBR1      Cytochrome b [cytb] [Camelus bactrianus (Bactrian camel)] 379 AA
Q8HBR1_CAMBA align

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Score = 754 bits (1948), Expect = 0.0
Identities = 365/379 (96%), Positives = 372/379 (98%)

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Query: 1  MTNIRKSHPLLKIMNDAFIDLPAISNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
          MTNIRKSHPLLKI+NDADFIDLPAISNISSWWNFGSLLG+CLIMQILTGLFLAMHYTSDTT
Sbjct: 1  MTNIRKSHPLLKIVNDAFIDLPAISNISSWWNFGSLLGICLIMQILTGLFLAMHYTSDTT 60

Query: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
          TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTF ETWNVG++LL
Sbjct: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFLETWNVGIILL 120

Query: 121 FTVMATAFMGVYLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180
          FTVMATAFMGVYLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA
Sbjct: 121 FTVMATAFMGVYLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLMLLALL 240
          FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALL+L LL
Sbjct: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLVLLILL 240

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Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLAL+LSILI
 Sbjct: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALILSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQVPEPPFIMIGQVASILYFS 360
 LA IP LHTSKQSRM FRPISQCLFWVLVADLLTLTWIGGQVPEPFI+IGQ ASILYFS
 Sbjct: 301 LALIPMLHTSKQRSMMFRPISQCLFWVLVADLLTLTWIGGQVPEPPFIVIGQAASILYFS 360

Query: 361 LILILMPVAGIENRILKW 379
 LILILMPVAGIENRILKW
 Sbjct: 361 LILILMPVAGIENRILKW 379

tr Q8HFA7 Cytochrome b [cytb] [Camelus bactrianus (Bactrian camel)] 379 AA
 Q8HFA7_CAMBA align

Score = 753 bits (1944), Expect = 0.0
 Identities = 364/379 (96%), Positives = 371/379 (97%)

Query: 1 MTNIRKSHPLLKIMNDAFIDLPAISNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
 MTN RKSHPLLKI+NDAFIDL PSNISSWWNFGSLLG+CLIMQILTGLFLAMHYTSDTT
 Sbjct: 1 MTNTRKSHPLLKIVNDAFIDLPTPSNISSWWNFGSLLGICLIMQILTGLFLAMHYTSDTT 60

Query: 61 TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
 TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTF ETWNVG++LL
 Sbjct: 61 TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFLETWNVGIILL 120

Query: 121 FTMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSDKATLTRFFA 180
 FTMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSDKATLTRFFA
 Sbjct: 121 FTMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSMDKIPFHPYYTIKDILGALLMLLALL 240
 FHFILPFIITALVAVHLLFLHETGSNNPTGISSMDKIPFHPYYTIKDILGALL+L LL
 Sbjct: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSMDKIPFHPYYTIKDILGALLLVLILL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLAL+LSILI
 Sbjct: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALILSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQVPEPPFIMIGQVASILYFS 360
 LA IP LHTSKQSRM FRPISQCLFWVLVADLLTLTWIGGQVPEPFI+IGQ ASILYFS
 Sbjct: 301 LALIPMLHTSKQRSMMFRPISQCLFWVLVADLLTLTWIGGQVPEPPFIVIGQAASILYFS 360

Query: 361 LILILMPVAGIENRILKW 379
 LILILMPVAGIENRILKW
 Sbjct: 361 LILILMPVAGIENRILKW 379

tr Q5GH08 Cytochrome b [cytb] [Lama glama argentina] 379 AA
 Q5GH08_LAMPA align

Score = 747 bits (1929), Expect = 0.0
 Identities = 358/379 (94%), Positives = 369/379 (97%)

Query: 1 MTNIRKSHPLLKIMNDAFIDLPAISNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
 MTNIRKSHPLLKI+N+AFIDLPAISNISSWWNFGSLLG+CLIMQI+TGLFLAMHYTSDTT
 Sbjct: 1 MTNIRKSHPLLKIVNNAFIDLPAISNISSWWNFGSLLGICLIMQIMTGLFLAMHYTSDTT 60

Query: 61 TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
 TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSY F ETWN+G++LL
 Sbjct: 61 TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYAFLETWNIIGIILL 120

Query: 121 FTMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSDKATLTRFFA 180
 FTMATAFMGYVLPWGQMSFWGATVITNLLSAIPY+GTTTLEWIWGGFSDKATLTRFFA
 Sbjct: 121 FTMATAFMGYVLPWGQMSFWGATVITNLLSAIPYVGTTLVEWIWGGFSDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSMDKIPFHPYYTIKDILGALLMLLALL 240
 FHFILPFI AL VHLLFLHETGSNNPTGISSMDKIPFHPYYTIKDILGALL+L LL
 Sbjct: 181 FHFILPFI IAALAGVHLLFLHETGSNNPTGISSMDKIPFHPYYTIKDILGALLLILILL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
 +LVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLAL+LSILI
 Sbjct: 241 LVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALILSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQVPEPPFIMIGQVASILYFS 360
 LAFIP LHTSKQSRM FRPISQCLFW LVADLLTLTWIGGQVPEPPFIMIGQVASILYFS
 Sbjct: 301 LAFIPLHTSKQRSMMFRPISQCLFWTLVADLLTLTWIGGQVPEPPFIMIGQVASILYFS 360

Query: 361 LILILMPVAGIENRILKW 379
 LILILMPVAGIEN ILKW

Sbjct: 361 LILILMPVAGIENHILKW 379

sp Q36227 Cytochrome b [MT-CYB] [Lama vicugna (Vicugna) (Vicugna vicugna)] 379 AA
CYB_LAMVI align

Score = 745 bits (1924), Expect = 0.0
Identities = 357/379 (94%), Positives = 368/379 (97%)

Query: 1 MTNIRKSHPLLKIMNDAFIDLPA P SNISSW NFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
MTNIRKSHPLLKI+N+AFIDLPA P SNISSW NFGSLLG+CLIMQI+TGLFLAMHYTSDTT
Sbjct: 1 MTNIRKSHPLLKIVNNAFIDLPA P SNISSW NFGSLLGICLIMQIMTGLFLAMHYTSDTT 60

Query: 61 TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSY F ETWN+G++LL
Sbjct: 61 TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYAFLETWNIGIILL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSDKATLTRFFA 180
FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPY+GTTLVEWIWGGFSDKATL RFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYVGTTLVEWIWGGFSDKATLNRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLMLLALL 240
FHFILPFI AL VHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALL+L LL
Sbjct: 181 FHFILPFI IAALAGVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLILILL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
+LVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLAL+LSILI
Sbjct: 241 LLVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALILSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQVPEPPFIMIGQVASILYFS 360
LAFIP LHTSKQRSM FRPISQCLFW LVADLLTLTWIGGQVPEPPFIMIGQVASILYFS
Sbjct: 301 LAFIPLLHTSKQRSMMFRPISQCLFWTLVADLLTLTWIGGQVPEPPFIMIGQVASILYFS 360

Query: 361 LILILMPVAGIENRILKW 379
LILILMPVAGIEN ILKW
Sbjct: 361 LILILMPVAGIENHILKW 379

sp Q34891 Cytochrome b [MT-CYB] [Lama glama (Llama)] 379 AA
CYB_LAMGL align

Score = 745 bits (1924), Expect = 0.0
Identities = 357/379 (94%), Positives = 368/379 (97%)

Query: 1 MTNIRKSHPLLKIMNDAFIDLPA P SNISSW NFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
MTNIRKSHPLLKI+N+AFIDLPA P SNISSW NFGSLLG+CLIMQI+TGLFLAMHYTSDTT
Sbjct: 1 MTNIRKSHPLLKIVNNAFIDLPA P SNISSW NFGSLLGICLIMQIMTGLFLAMHYTSDTT 60

Query: 61 TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSY F ETWN+G++LL
Sbjct: 61 TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYAFLETWNIGIILL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSDKATLTRFFA 180
FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPY+GTTLVEWIWGGFSDKATL RFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYVGTTLVEWIWGGFSDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLMLLALL 240
FHFILPF+I AL VHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALL+L LL
Sbjct: 181 FHFILPFVIAALAGVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLILTLL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
+LVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI
Sbjct: 241 LLVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQVPEPPFIMIGQVASILYFS 360
LA IP LHTSKQRSM FRPISQCLFW LVADLLTLTWIGGQVPEPPFIMIGQVASILYFS
Sbjct: 301 LALIPLHTSKQRSMMFRPISQCLFWTLVADLLTLTWIGGQVPEPPFIMIGQVASILYFS 360

Query: 361 LILILMPVAGIENRILKW 379
LILILMPVAGIEN ILKW
Sbjct: 361 LILILMPVAGIENHILKW 379

tr Q5GH03 Cytochrome b [cytb] [Lama guanicoe huanacus] 379 AA
Q5GH03_LAMGU align

Score = 745 bits (1924), Expect = 0.0
Identities = 357/379 (94%), Positives = 368/379 (97%)

Query:	1	MTNIRKSHPLLKIMNDAFIDLPA	SNISSWWNF	SGSLGVL	IMQILTGLFLAMHYTSDTT	60
Sbjct:	1	MTNIRKSHPLLKI+N+AFIDLPA	SNISSWWNF	SGSLG+CLIMQI+TGLFLAMHYTSDTT		60
Query:	61	TAFSSVAHICRDVNYGWIIRYL	HANGASMPFICLYIHVGRGLY	GSYTFSETNVN	GMVLL	120
Sbjct:	61	TAFSSVAHICRDVNYGWIIRYL	HANGASMPFICLYIHVGRGLY	GSYAFLETWNIGIILL		120
Query:	121	FTVMATAFMGYVLPWGQMSF	WGATVITNLLSAIPYIGTTL	VEWIWGGFSDKATLTRFFA		180
Sbjct:	121	FTVMATAFMGYVLPWGQMSF	WGATVITNLLSAIPY+GTTL	VEWIWGGFSDKATLTRFFA		180
Query:	181	FHFILPFIITALVAVHLLFL	HETGSNNPTGISSDMDKIP	PHPYTTIKDILGALLMLALL		240
Sbjct:	181	FHFILFP+I AL VHLFLHETGS	NNPTGISSDMDKIPHPYTTIKDILGALL+L LL			240
Query:	241	ILVLFSPDLLGDPDNYTPAN	PLNTPPHIKPEWYFLFAYAILRSIPN	LKGGVLALVLSILI		300
Sbjct:	241	LLVLFSPDLLGDPDNYTPAN	PLNTPPHIKPEWYFLFAYAILRSIPN	LKGGVLALVLSILI		300
Query:	301	LAFIPALHTSKQRSMTFRPIS	QSCFLFWLVADLLTLTWIGQP	VEPPFIMIGQVASILYFS		360
Sbjct:	301	LALIPLLHTSKQSRMMFRPIS	QSCFLFWLTADLLTLTWIGQP	VEPPFIMIGQVASILYFS		360
Query:	361	LILILMPVAGIIENRILKW			379	
Sbjct:	361	LILILMPVAGIENILKW			379	

| tr | Q5GH04 | Cytochrome b [cytb] | [Lama guanicoe cacsilensis] | 379 AA |
| | Q5GH04 LAMGU | | | align |

Score = 745 bits (1924), Expect = 0.0
Identities = 357/379 (94%), Positives = 368/379 (97%)

Query: 1	MTNIRKSHPLLKIMNDAFIDLPA	SNISSWWNF	GSLLGVCLIMQIL	TGLFLAMHYTSDTT	60
Sbjct: 1	MTNIRKSHPLLKI+N+AFIDLPA	SNISSWWNF	GSLLG+CLIMQI+TGLFLAMHYTSDTT		60
Query: 61	TAFSSVAHICRDVNYGWIIRYL	HANGASMF	FFICLYIHVGRGLYGSY	TFSETNVNVMVLL	120
Sbjct: 61	TAFSSVAHICRDVNYGWIIRYL	HANGASMF	FFICLYIHVGRGLYGSY	F ETWN+G++LL	120
Query: 121	FTVMATAFMGYVLPWQMG	SFWGATVITNLLSAIPY	IGTTLVEW	IWGGFSDVKATLTRFFA	180
Sbjct: 121	FTVMATAFMGYVLPWQMG	SFWGATVITNLLSAIPY	+GTTTLEW	IWGGFSDVKATLTRFFA	180
Query: 181	FHFILPFIITALVAVHLLFL	HETGSNNPTGISSDMDKI	PFHPYYTIKDILGALLLMLALL		240
Sbjct: 181	FHFILPF+I AL VHLFL	HETGSNNPTGISSDMDKI	PFHPYYTIKDILGALLL+L LL		240
Query: 241	LILVLFSPDLLGDPDNYTPAN	PLNTPPHIKPEWYFLFAYAILRS	IPNKLGGVLA	LVLVSILI	300
Sbjct: 241	LILVLFSPDLLGDPDNYTPAN	PLNTPPHIKPEWYFLFAYAILRS	IPNKLGGVLA	LVLVSILI	300
Query: 301	LAFIPALHTSKQRSMTFRPIS	QCLFWVLADLLTLTWIGGQ	PVPEPPFIMIGQVASILYFS		360
Sbjct: 301	LALIPLLHTSKQSRSMFRPIS	QCLFWT	LVLADLLTLTWIGGQ	PVPEPPFIMIGQVASILYFS	360
Query: 361	LILILMPVAGIIENRI	LKW			379
Sbjct: 361	LILILMPVAGIIENILK	W			379

```
tr  Q70LJ9      Cytochrome b [cytb] [Lama guanicoe pacos (Alpaca) (Lama pacos)] 379 AA
      Q70LJ9 LAMPA                                         align
```

Score = 745 bits (1924), Expect = 0.0
Identities = 357/379 (94%), Positives = 368/379 (97%)

Query: 1	MTNIRKSHPELLKIMNDAPIDLPA	PSNIS	SSWWNF	SGLLG	VCILIMQIL	TGLFLAMHYTSDTT	60
	MTNIRKSHPELLKI+N	A	FIDLPA	SNIS	SSWWNF	SGLLG+CLIMQI+TGLFLAMHYTSDTT	
Sbjct: 1	MTNIRKSHPELLKIVNNA	FDICL	PA	SNIS	SSWWNF	SGLLGICLIMQIMTGLFLAMHYTSDTT	60
Query: 61	TAFSSVAHICRDVNYGWI	I	RYLHANGA	SMFP	ICLYIHVGRGLY	YGSYTFSETNWNVMVLL	120
	TAFSSVAHICRDVNYGWI	I	RYLHANGA	SMFP	ICLYIHVGRGLY	YGSYF ETWN+G+LL	
Sbjct: 61	TAFSSVAHICRDVNYGWI	I	RYLHANGA	SMFP	ICLYIHVGRGLY	YGSYAFLETWNIGI+LL	120

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Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180
          FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPY+GTTLVEWIWGGFSVDKATLTRFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYVGTTLVEWIWGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLMLALL 240
          FHFILPFI+I AL VHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALL+L LL
Sbjct: 181 FHFILPFIIVAAALAGVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLILTL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
          +LVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI
Sbjct: 241 LLVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQVPEPPFIMIGQVASILYFS 360
          LA IP LHTSKQSRM FRPISQCLFW LVADLLTLTWIGGQVPEPPFIMIGQVASILYFS
Sbjct: 301 LALIPLLHTSKQRSMMFRPISQCLFWTLVADLLTLTWIGGQVPEPPFIMIGQVASILYFS 360

Query: 361 LILILMPVAGIENRILKW 379
          LILILMPVAGIEN ILKW
Sbjct: 361 LILILMPVAGIENHILKW 379

```

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sp Q34916      Cytochrome b [MT-CYB] [Lama guanicoe pacos (Alpaca) (Lama pacos)] 379 AA
          CYB_LAMPA align

```

Score = 744 bits (1920), Expect = 0.0
Identities = 357/379 (94%), Positives = 368/379 (97%)

```

Query: 1  MTNIRKSHPLLKIMNDAFIDLPAISNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
          MTNIRKSHPLLKI+N+AFIDLPAISNISSWWNFGSLLG+CLIMQI+TGLFLAMHYTSDTT
Sbjct: 1  MTNIRKSHPLLKIVNNAFIDLPAISNISSWWNFGSLLGICLIMQIMTGLFLAMHYTSDTT 60

Query: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
          TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSY F ETWN+G++LL
Sbjct: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYAFLETWNIGIILL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180
          FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPY+GTTLVEWIWGGFSVDKATLTRFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYVGTTLVEWIWGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLMLALL 240
          FHFILPFI+I AL VHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALL+L LL
Sbjct: 181 FHFILPFIIVAAALAGVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLILIL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
          +LVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLAL+LSILI
Sbjct: 241 LLVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALILSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQVPEPPFIMIGQVASILYFS 360
          LAFIP LHTSKQSRM FRPISQCLFW LVADLLTLTWIGGQVPEPPFIMIGQVASIL FS
Sbjct: 301 LALIPLLHTSKQRSMMFRPISQCLFWTLVADLLTLTWIGGQVPEPPFIMIGQVASILSFS 360

Query: 361 LILILMPVAGIENRILKW 379
          LILILMPVAGIEN ILKW
Sbjct: 361 LILILMPVAGIENHILKW 379

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tr Q5GH09      Cytochrome b [cytb] [Lama glama chaku] 379 AA
          Q5GH09_LAMPA align

```

Score = 744 bits (1920), Expect = 0.0
Identities = 356/379 (93%), Positives = 367/379 (96%)

```

Query: 1  MTNIRKSHPLLKIMNDAFIDLPAISNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
          MTNIRKSHPLLKI+N+AFIDLPAISNISSWWNFGSLLG+CLIMQI+TGLFLAMHYTSDTT
Sbjct: 1  MTNIRKSHPLLKIVNNAFIDLPAISNISSWWNFGSLLGICLIMQIMTGLFLAMHYTSDTT 60

Query: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
          TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSY F ETWN+G++LL
Sbjct: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYAFLETWNIGIILL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180
          FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPY+GTTLVEWIWGGFSVDKATLTRFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYVGTTLVEWIWGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLMLALL 240
          FHFILPFI+I AL VHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILG LLL+L LL
Sbjct: 181 FHFILPFIIVAAALAGVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGVLLLILTL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
          +LVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI

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Sbjct: 241 LLVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQVVEPPFIMIGQVASILYFS 360
LA IP LHTSKQSRM FRPISQCLFW LVADLLTLTWIGGQVVEPPFIMIGQVASILYFS

Sbjct: 301 LALIPLLLHTSKQRSMMFRPISQCLFWTLVADLLTLTWIGGQVVEPPFIMIGQVASILYFS 360

Query: 361 LILILMPVAGIIEENRILKW 379
LILILMPVAGIIEEN ILKW

Sbjct: 361 LILILMPVAGIIEENHILKW 379

tr Q5GH11 Cytochrome b [cytb] [Lama pacos suri] 379 AA
Q5GH11_LAMPA align

Score = 744 bits (1920), Expect = 0.0
Identities = 356/379 (93%), Positives = 367/379 (96%)

Query: 1 MTNIRKSHPLLKIMNDAFIDLPAISNWSNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
MTNIRKSHPLLKIN+AFIDLPAISNWSNFGSLLG+CLIMQI+TGLFLAMHYTSDTT

Sbjct: 1 MTNIRKSHPLLKIVNNAFIDLPAISNWSNFGSLLGICLIMQIMTGLFLAMHYTSDTT 60

Query: 61 TAFSSVAHICRDVNYGWIIRYLHANGASMPFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
TAFSSVAHICRDVNYGWIIRYLHANGASMPFFICLYIHVGRGLYYGSY F ETWN+G++LL

Sbjct: 61 TAFSSVAHICRDVNYGWIIRYLHANGASMPFFICLYIHVGRGLYYGSYAFLETWNIGIILL 120

Query: 121 FTVMATAFMGYVLPWQMSFWGATVITNLLSAIPYIGTTLVEIWWGGFSVDKATLTRFFA 180
FTVMATAFMGYVLPWQMSFWGATVITNLLSAIPY+GTTTVEIWWGGFSVDKATLTRFFA

Sbjct: 121 FTVMATAFMGYVLPWQMSFWGATVITNLLSAIPYVGTTLVEIWWGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSMDKIPFHPYYTIKDILGALLMLALL 240
FHFILPF+I AL VHLFLHETGSNNPTGISSMDKIPFHPYYTIKDILG LLL+L LL

Sbjct: 181 FHFILPFVIAALAGVHLFLHETGSNNPTGISSMDKIPFHPYYTIKDILGVLLLILTL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
+LVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI

Sbjct: 241 LLVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQVVEPPFIMIGQVASILYFS 360
LA IP LHTSKQSRM FRPISQCLFW LVADLLTLTWIGGQVVEPPFIMIGQVASILYFS

Sbjct: 301 LALIPLLLHTSKQRSMMFRPISQCLFWTLVADLLTLTWIGGQVVEPPFIMIGQVASILYFS 360

Query: 361 LILILMPVAGIIEENRILKW 379
LILILMPVAGIIEEN ILKW

Sbjct: 361 LILILMPVAGIIEENHILKW 379

tr Q5GH06 Cytochrome b [cytb] [Lama guanicoe cacsilensis] 379 AA
Q5GH06_LAMGU align

Score = 743 bits (1917), Expect = 0.0
Identities = 355/379 (93%), Positives = 367/379 (96%)

Query: 1 MTNIRKSHPLLKIMNDAFIDLPAISNWSNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
MTNIRKSHPLLKIN+A+IDLPAISNWSNFGSLLG+CLIMQI+TGLFLAMHYTSDTT

Sbjct: 1 MTNIRKSHPLLKIVNNAYIDLPAISNWSNFGSLLGICLIMQIMTGLFLAMHYTSDTT 60

Query: 61 TAFSSVAHICRDVNYGWIIRYLHANGASMPFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
TAFSSVAHICRDVNYGWIIRYLHANGASMPFFICLYIHVGRGLYYGSY F ETWN+G++LL

Sbjct: 61 TAFSSVAHICRDVNYGWIIRYLHANGASMPFFICLYIHVGRGLYYGSYAFLETWNIGIILL 120

Query: 121 FTVMATAFMGYVLPWQMSFWGATVITNLLSAIPYIGTTLVEIWWGGFSVDKATLTRFFA 180
FTVMATAFMGYVLPWQMSFWGATVITNLLSAIPY+GTTTVEIWWGGFSVDKATLTRFFA

Sbjct: 121 FTVMATAFMGYVLPWQMSFWGATVITNLLSAIPYVGTTLVEIWWGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSMDKIPFHPYYTIKDILGALLMLALL 240
FHFILPF+I AL VHLFLHETGSNNPTGISSMDKIPFHPYYTIKDILG LLL+L LL

Sbjct: 181 FHFILPFVIAALAGVHLFLHETGSNNPTGISSMDKIPFHPYYTIKDILGVLLLILTL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
+LVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI

Sbjct: 241 LLVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQVVEPPFIMIGQVASILYFS 360
LA IP LHTSKQSRM FRPISQCLFW LVADLLTLTWIGGQVVEPPFIMIGQVASILYFS

Sbjct: 301 LALIPLLLHTSKQRSMMFRPISQCLFWTLVADLLTLTWIGGQVVEPPFIMIGQVASILYFS 360

Query: 361 LILILMPVAGIIEENRILKW 379
LILILMPVAGIIEEN ILKW

Sbjct: 361 LILILMPVAGIIEENHILKW 379

sp Q34890 Cytochrome b [MT-CYB] [Lama guanicoe (Guanaco)] 379 AA
CYB_LAMGU align

Score = 742 bits (1915), Expect = 0.0
Identities = 355/379 (93%), Positives = 366/379 (96%)

```
Query: 1  MTNIRKSHPLLKIMNDAFIDLPAAPSNISWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
          MTNIRKSHPLLKI+N+AFIDLPAAPSNISWWNFGSLLG+CLIMQI+TGLFLAMHYTSDT
Sbjct: 1  MTNIRKSHPLLKIVNNAFIDLPAAPSNISWWNFGSLLGICLIMQIMTGLFLAMHYTSDTA 60

Query: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
          TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSY F ETWN+G++LL
Sbjct: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYAFLETWNIGIILL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180
          FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPY+GTTLVEWIWGGFSVDKATLTRFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYVGTTLVEWIWGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLMLLALL 240
          FHFILPF+I AL VHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILG LLL+L LL
Sbjct: 181 FHFILPFVIAALAGVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGVLLLIITLL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
          +LVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI
Sbjct: 241 LLVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360
          LA IP LHTSKQSRM FRPISQCLFW LVADLLTLTWIGGQPVEPPFIMIGQVASILYFS
Sbjct: 301 LALIPLLHTSKQRSMMFRPISQCLFWTLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360

Query: 361 LILILMPVAGIENRILKW 379
          LILILMPVAGIEN ILKW
Sbjct: 361 LILILMPVAGIENHILKW 379
```

tr Q5GH02 Cytochrome b [cytb] [Lama guanicoe huanacus] 379 AA
Q5GH02_LAMGU align

Score = 742 bits (1915), Expect = 0.0
Identities = 355/379 (93%), Positives = 366/379 (96%)

```
Query: 1  MTNIRKSHPLLKIMNDAFIDLPAAPSNISWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
          MTNIRKSHPLLKI+N+AFIDLPAAPSNISWWNFGSLLG+CLIMQI+TGLFLAMHYTSDT
Sbjct: 1  MTNIRKSHPLLKIVNNAFIDLPAAPSNISWWNFGSLLGICLIMQIMTGLFLAMHYTSDTA 60

Query: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
          TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSY F ETWN+G++LL
Sbjct: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYAFLETWNIGIILL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180
          FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPY+GTTLVEWIWGGFSVDKATLTRFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYVGTTLVEWIWGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLMLLALL 240
          FHFILPF+I AL VHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILG LLL+L LL
Sbjct: 181 FHFILPFVIAALAGVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGVLLLIITLL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
          +LVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI
Sbjct: 241 LLVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360
          LA IP LHTSKQSRM FRPISQCLFW LVADLLTLTWIGGQPVEPPFIMIGQVASILYFS
Sbjct: 301 LALIPLLHTSKQRSMMFRPISQCLFWTLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360

Query: 361 LILILMPVAGIENRILKW 379
          LILILMPVAGIEN ILKW
Sbjct: 361 LILILMPVAGIENHILKW 379
```

tr Q5GGY6 Cytochrome b [cytb] [Lama guanicoe guanicoe] 379 AA
Q5GGY6_LAMGU align

Score = 742 bits (1915), Expect = 0.0
Identities = 355/379 (93%), Positives = 366/379 (96%)

```
Query: 1  MTNIRKSHPLLKIMNDAFIDLPAAPSNISWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
          MTNIRKSHPLLKI+N+AFIDLPAAPSNISWWNFGSLLG+CLIMQI+TGLFLAMHYTSDT
Sbjct: 1  MTNIRKSHPLLKIVNNAFIDLPAAPSNISWWNFGSLLGICLIMQIMTGLFLAMHYTSDTA 60
```

```

Query: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
          TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSY F ETWN+G++LL
Sbjct: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYAFLETWNIGIILL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSDKATLTRFFA 180
          FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPY+GTTLVEWIWGGFSDKATLTRFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYVGTTLVEWIWGGFSDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLMLLALL 240
          FHFILPF+I AL VHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILG LLL+L LL
Sbjct: 181 FHFILPFVIAALAGVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGVLLLILTL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
          +LVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI
Sbjct: 241 LLVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQVPEPPFIMIGQVASILYFS 360
          LA IP LHTSKQSRM FRPISQCLFW LVADLLTLTWIGGQVPEPPFIMIGQVASILYFS
Sbjct: 301 LALIPLLHTSKQRSMMFRPISQCLFWTLVADLLTLTWIGGQVPEPPFIMIGQVASILYFS 360

Query: 361 LILILMPVAGIENRILKW 379
          LILILMPVAGIEN ILKW
Sbjct: 361 LILILMPVAGIENHILKW 379

```

```

tr Q5GH05      Cytochrome b [cytb] [Lama guanicoe cacsilensis] 379 AA
Q5GH05_LAMGU align

```

Score = 742 bits (1915), Expect = 0.0
 Identities = 355/379 (93%), Positives = 366/379 (96%)

```

Query: 1  MTNIRKSHPLLKIMNDAFIDLPAISNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
          MTNIRKSHPLLKI+N+AFIDLPAISNISSWWNFGSLLG+CLIMQI+TGLFLAMHYTSDT
Sbjct: 1  MTNIRKSHPLLKIVNNAFIDLPAISNISSWWNFGSLLGICLIMQIMTGLFLAMHYTSDTA 60

Query: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
          TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSY F ETWN+G++LL
Sbjct: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYAFLETWNIGIILL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSDKATLTRFFA 180
          FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPY+GTTLVEWIWGGFSDKATLTRFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYVGTTLVEWIWGGFSDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLMLLALL 240
          FHFILPF+I AL VHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILG LLL+L LL
Sbjct: 181 FHFILPFVIAALAGVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGVLLLILTL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
          +LVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI
Sbjct: 241 LLVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQVPEPPFIMIGQVASILYFS 360
          LA IP LHTSKQSRM FRPISQCLFW LVADLLTLTWIGGQVPEPPFIMIGQVASILYFS
Sbjct: 301 LALIPLLHTSKQRSMMFRPISQCLFWTLVADLLTLTWIGGQVPEPPFIMIGQVASILYFS 360

Query: 361 LILILMPVAGIENRILKW 379
          LILILMPVAGIEN ILKW
Sbjct: 361 LILILMPVAGIENHILKW 379

```

```

tr Q5GGY0      Cytochrome b [cytb] [Lama guanicoe guanicoe] 379 AA
Q5GGY0_LAMGU align

```

Score = 741 bits (1914), Expect = 0.0
 Identities = 355/379 (93%), Positives = 366/379 (96%)

```

Query: 1  MTNIRKSHPLLKIMNDAFIDLPAISNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
          MTNIRKSHPLLKI+N+AFIDLPAISNISSWWNFGSLLG+CLIMQI+TGLFLAMHYTSDT
Sbjct: 1  MTNIRKSHPLLKIVNNAFIDLPAISNISSWWNFGSLLGICLIMQIMTGLFLAMHYTSDTA 60

Query: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
          TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSY F ETWN+G++LL
Sbjct: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYAFLETWNIGIILL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSDKATLTRFFA 180
          FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPY+GTTLVEWIWGGFSDKATLTRFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYLGTTLVEWIWGGFSDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLMLLALL 240
          FHFILPF+I AL VHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILG LLL+L LL

```

Sbjct: 181 FHFILPFVIAALAGVHLLFLHETGSNNPTGISSMDKIPFHPYYTIKDILGVLLILTL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
+LVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI

Sbjct: 241 LLVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQVPEPPFIMIGQVASILYFS 360
LA IP LHTSKQSRM FRPISQCLFW LVADLLTLTWIGGQVPEPPFIMIGQVASILYFS

Sbjct: 301 LALIPLLHTSKQRSMMFRPISQCLFWTLVADLLTLTWIGGQVPEPPFIMIGQVASILYFS 360

Query: 361 LILILMPVAGIENRILKW 379
LILILMPVAGIEN ILKW

Sbjct: 361 LILILMPVAGIENHILKW 379

tr 003364 Cytochrome b [Lama guanicoe (Guanaco)] 379 AA
003364_LAMGU align

Score = 741 bits (1913), Expect = 0.0
Identities = 355/379 (93%), Positives = 366/379 (96%)

Query: 1 MTNIRKSHPLLKIMNDAFIDLPAISNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
MTNIRKSHPLLKI+N+AFIDLPAISNISSWWNFGSLLG+CLIMQI+TGLFLAMHYTSDT

Sbjct: 1 MTNIRKSHPLLKIVNNAFIDLPAISNISSWWNFGSLLGICLIMQIMTGLFLAMHYTSDTA 60

Query: 61 TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSY F ETWN+G++LL

Sbjct: 61 TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYAFLETWNIGIILL 120

Query: 121 FTMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSDKATLTRFFA 180
FTMATAFMGYVLPWGQMSFWGATVITNLLSAIPY+GTTLVEWIWGGFSDKATLTRFFA

Sbjct: 121 FTMATAFMGYVLPWGQMSFWGATVITNLLSAIPYVGTTLVEWIWGGFSDKATLTRFFA 180

Query: 181 FHFILPFIITAVVHLLFLHETGSNNPTGISSMDKIPFHPYYTIKDILGALLLMLALL 240
FHFILPF+I AL VHLLFLHETGSNNPTGISSMDKIPFHPYYTIKDILG LLL+L LL

Sbjct: 181 FHFILPFVIAALAGVHLLFLHETGSNNPTGISSMDKIPFHPYYTIKDILGVLLILTL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
+LVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI

Sbjct: 241 LLVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQVPEPPFIMIGQVASILYFS 360
LA IP LHTSKQSRM FRPISQCLFW LVADLLTLTWIGGQVPEPPFIMIGQVASILYFS

Sbjct: 301 LALIPLLHTSKQRSMMFRPISQCLFWTLVADLLTLTWIGGQVPEPPFIMIGQVASILYFS 360

Query: 361 LILILMPVAGIENRILKW 379
LILILMPVAGIEN ILKW

Sbjct: 361 LILILMPVAGIENYILKW 379

tr Q5GGZ3 Cytochrome b [cytb] [Lama guanicoe huanacus] 379 AA
Q5GGZ3_LAMGU align

Score = 741 bits (1912), Expect = 0.0
Identities = 355/379 (93%), Positives = 366/379 (96%)

Query: 1 MTNIRKSHPLLKIMNDAFIDLPAISNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
MTNIRKSHPLLKI+N+AFIDLPAISNISSWWNFGSLLG+CLIMQI+TGLFLAMHYTSDTT

Sbjct: 1 MTNIRKSHPLLKIVNNAFIDLPAISNISSWWNFGSLLGICLIMQIMTGLFLAMHYTSDTT 60

Query: 61 TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSY F ETWN+G++LL

Sbjct: 61 TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYAFLETWNIGIILL 120

Query: 121 FTMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSDKATLTRFFA 180
FTMATAFMGYVLPWGQMSFWGA VITNLLSAIPY+GT LVEWIWGGFSDKATLTRFFA

Sbjct: 121 FTMATAFMGYVLPWGQMSFWGAPVITNLLSAIPYVGTPLVEWIWGGFSDKATLTRFFA 180

Query: 181 FHFILPFIITAVVHLLFLHETGSNNPTGISSMDKIPFHPYYTIKDILGALLLMLALL 240
FHFILPF+I AL VHLLFLHETGSNNPTGISSMDKIPFHPYYTIKDILGALL+L LL

Sbjct: 181 FHFILPFVIAALAGVHLLFLHETGSNNPTGISSMDKIPFHPYYTIKDILGALLLILTL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
+LVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI

Sbjct: 241 LLVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQVPEPPFIMIGQVASILYFS 360
LA IP LHTSKQSRM FRPISQCLFW LVADLLTLTWIGGQVPEPPFIMIGQVASILYFS

Sbjct: 301 LALIPLLHTSKQRSMMFRPISQCLFWTLVADLLTLTWIGGQVPEPPFIMIGQVASILYFS 360

Query: 361 LILILMPVAGIENRILKW 379

LILILMPVAGIEN ILKW
 Sbjct: 361 LILILMPVAGIENHILKW 379

tr Q5GGY2 Cytochrome b [cytb] [Lama guanicoe guanicoe] 379 AA
 Q5GGY2_LAMGU align

Score = 741 bits (1912), Expect = 0.0
 Identities = 354/379 (93%), Positives = 366/379 (96%)

Query: 1 MTNIRKSHPLLKIMNDAFIDLPAISNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
 MTNIRKSHPLLLKI+N+AFIDLPAISNISSWWNFGSLLG+CLIMQI+TGLFLAMHYTSDT
 Sbjct: 1 MTNIRKSHPLLKIVNNAFIDLPAISNISSWWNFGSLLGICLIMQIMTGLFLAMHYTSDTA 60

Query: 61 TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
 TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSY F ETWN+G++LL
 Sbjct: 61 TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYAFLETWNIGIILL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSDKATLTRFFA 180
 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPY+GTTLVEWIWGGFSDKATLTRFFA
 Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYVGTTLVEWIWGGFSDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSMDKIPFHPYYTIKDILGALLMLLALL 240
 FHFILPFI+I AL VHLLFLHETGSNNPTGISSMDKIPFHPYYTIKDILG LLL+L LL
 Sbjct: 181 FHFILPFIIVIAALAGVHLLFLHETGSNNPTGISSMDKIPFHPYYTIKDILGVLLLILTL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
 +LVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI
 Sbjct: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWLVADLLTLTWIGGQVPEPPFIMIGQVASILYFS 360
 LA IP LHTSKQSRM FRPISQCLFW LVADLLTLTWIGGQVPEPPFIM+GQVASILYFS
 Sbjct: 301 LALIPLLHTSKQRSMMFRPISQCLFWTLVADLLTLTWIGGQVPEPPFIMMGQVASILYFS 360

Query: 361 LILILMPVAGIENRILKW 379
 LILILMPVAGIEN ILKW
 Sbjct: 361 LILILMPVAGIENHILKW 379

tr Q5GGZ7 Cytochrome b [cytb] [Lama guanicoe huanacus] 379 AA
 Q5GGZ7_LAMGU align

Score = 740 bits (1911), Expect = 0.0
 Identities = 354/379 (93%), Positives = 365/379 (96%)

Query: 1 MTNIRKSHPLLKIMNDAFIDLPAISNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
 MTNIRKSHPLLLKI+N+AFIDL PISNISSWWNFGSLLG+CLIMQI+TGLFLAMHYTSDT
 Sbjct: 1 MTNIRKSHPLLKIVNNAFIDLPTPSNISSWWNFGSLLGICLIMQIMTGLFLAMHYTSDTA 60

Query: 61 TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
 TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSY F ETWN+G++LL
 Sbjct: 61 TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYAFLETWNIGIILL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSDKATLTRFFA 180
 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPY+GTTLVEWIWGGFSDKATLTRFFA
 Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYVGTTLVEWIWGGFSDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSMDKIPFHPYYTIKDILGALLMLLALL 240
 FHFILPFI+I AL VHLLFLHETGSNNPTGISSMDKIPFHPYYTIKDILG LLL+L LL
 Sbjct: 181 FHFILPFIIVIAALAGVHLLFLHETGSNNPTGISSMDKIPFHPYYTIKDILGVLLLILTL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
 +LVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI
 Sbjct: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWLVADLLTLTWIGGQVPEPPFIMIGQVASILYFS 360
 LA IP LHTSKQSRM FRPISQCLFW LVADLLTLTWIGGQVPEPPFIMIGQVASILYFS
 Sbjct: 301 LALIPLLHTSKQRSMMFRPISQCLFWTLVADLLTLTWIGGQVPEPPFIMIGQVASILYFS 360

Query: 361 LILILMPVAGIENRILKW 379
 LILILMPVAGIEN ILKW
 Sbjct: 361 LILILMPVAGIENHILKW 379

tr Q5GH07 Cytochrome b [cytb] [Vicugna vicugna mensalis] 379 AA
 Q5GH07_LAMVI align

Score = 739 bits (1908), Expect = 0.0
Identities = 355/379 (93%), Positives = 366/379 (96%)

```
Query: 1  MTNIRKSHPLLKIMNDAFIDLPAISNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
          MTN  RKSHPL LKI+N+AFIDLPAISNISSWWNFGSLLG+CLIMQI+TGLFLAMHYTSDTT
Sbjct: 1  MTNIRKSHPLKIVNNAFIDLPAISNISSWWNFGSLLGICLIMQIMTGLFLAMHYTSDTT 60

Query: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
          TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYI  VGRGLYYGSY F ETWN+G++LL
Sbjct: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIFVGRGLYYGSYAFLETWNIGIILL 120

Query: 121  FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWINGGFSVDKATLTRFFA 180
          FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPY+GTTLVEWINGGFSVDKATLTRFFA
Sbjct: 121  FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYVGTTLVEWINGGFSVDKATLTRFFA 180

Query: 181  FHFILPFIITALVAVHLLFLHETGSNNPTGISSMDKIPFHPYYTIKDILGALLMLALL 240
          FHFILPFI I AL  VHLLFLHETGSNNPTGISSMDKIPFHPYYTIKDILGALL+L LL
Sbjct: 181  FHFILPFI AALAGVHLLFLHETGSNNPTGISSMDKIPFHPYYTIKDILGALLLILILL 240

Query: 241  ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLAIVLSILI 300
          +LVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLAIVLSILI
Sbjct: 241  LVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLAIVLSILI 300

Query: 301  LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQVPEPPFIMIGQVASILYFS 360
          LAFIP LHTSKQSRM FRPISQCLFW LVADLLTLTWIGGQVPEPPFIMIGQVASILYFS
Sbjct: 301  LAFIPLHTSKQRSMMFRPISQCLFWTLVADLLTLTWIGGQVPEPPFIMIGQVASILYFS 360

Query: 361  LILILMPVAGIENRILKW 379
          LILILMPVAGIEN ILKW
Sbjct: 361  LILILMPVAGIENHILKW 379
```

tr Q5GGY8 Cytochrome b [cytb] [Lama guanicoe huanacus] 379 AA
Q5GGY8_LAMGU align

Score = 739 bits (1907), Expect = 0.0
Identities = 354/379 (93%), Positives = 365/379 (96%)

```
Query: 1  MTNIRKSHPLLKIMNDAFIDLPAISNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
          MTNIRKSHPL LKI+N+AFIDLPAISNISSWWNFGSLLG+CLIMQI+TGLFLAMHYTSDT
Sbjct: 1  MTNIRKSHPLKIVNNAFIDLPAISNISSWWNFGSLLGICLIMQIMTGLFLAMHYTSDTA 60

Query: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
          TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSY F ETWN+G++LL
Sbjct: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYAFLETWNIGIILL 120

Query: 121  FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWINGGFSVDKATLTRFFA 180
          FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPY+GTTLVEWINGGFSVDKATLTRFFA
Sbjct: 121  FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYVGTTLVEWINGGFSVDKATLTRFFA 180

Query: 181  FHFILPFIITALVAVHLLFLHETGSNNPTGISSMDKIPFHPYYTIKDILGALLMLALL 240
          FHFILPFI+I AL  VHLLFLHETGSNNPTGISSMD KIPFHPYYTIKDILG LLL+L LL
Sbjct: 181  FHFILPFI AALAGVHLLFLHETGSNNPTGISSMDAKIPFHPYYTIKDILGVLLLILTL 240

Query: 241  ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLAIVLSILI 300
          +LVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLAIVLSILI
Sbjct: 241  LVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLAIVLSILI 300

Query: 301  LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQVPEPPFIMIGQVASILYFS 360
          LA IP LHTSKQSRM FRPISQCLFW LVADLLTLTWIGGQVPEPPFIMIGQVASILYFS
Sbjct: 301  LALIPLHTSKQRSMMFRPISQCLFWTLVADLLTLTWIGGQVPEPPFIMIGQVASILYFS 360

Query: 361  LILILMPVAGIENRILKW 379
          LILILMPVAGIEN ILKW
Sbjct: 361  LILILMPVAGIENHILKW 379
```

tr Q5GGY9 Cytochrome b [cytb] [Lama guanicoe huanacus] 379 AA
Q5GGY9_LAMGU align

Score = 738 bits (1904), Expect = 0.0
Identities = 353/379 (93%), Positives = 364/379 (96%)

```
Query: 1  MTNIRKSHPLLKIMNDAFIDLPAISNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
          MTNIRKSHPL LKI+N+AFIDLPAISNISSWWNFGSLLG+CLIMQI+TGLFLAMHYTSDT
Sbjct: 1  MTNIRKSHPLKIVNNAFIDLPAISNISSWWNFGSLLGICLIMQIMTGLFLAMHYTSDTA 60

Query: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
          TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSY F ETWN+G++LL
Sbjct: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYAFLETWNIGIILL 120
```

```

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180
          FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPY+GTTLVEWIWGGFSVDKATLTRFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYVGTTLVEWIWGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLMLLALL 240
          FHFILPF+I AL VHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILG LLL+L LL
Sbjct: 181 FHFILPFVIAALAGVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGVLLLILTL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
          +LVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI
Sbjct: 241 LLVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360
          L IP LHTSKQSRM FRPISQCLFW LVADLLTLTWIGGQPVEPPFIMIGQVASILY S
Sbjct: 301 LPLIPLLHTSKQRSMMFRPISQCLFWTLVADLLTLTWIGGQPVEPPFIMIGQVASILYLS 360

Query: 361 LILILMPVAGIENRILKW 379
          LILILMPVAGIEN ILKW
Sbjct: 361 LILILMPVAGIENHILKW 379

```

sp Q5BQG9 Cytochrome b [MT-CYB] [Sus philippensis (Philippine warty pig)] 379 AA
CYB_SUSPH align

Score = 723 bits (1866), Expect = 0.0
Identities = 343/379 (90%), Positives = 363/379 (95%)

```

Query: 1 MTNIRKSHPLKIMNDAFIDLPAISNISSWVNFSGLLGVCLIMQILTGLFLAMHYTSDTT 60
          MTNIRKSHPL+KI+N+AFIDLPAISNISSWVNFSGLLG+CLI+QILTGLFLAMHYTSDTT
Sbjct: 1 MTNIRKSHPLMKIINNDAFIDLPAISNISSWVNFSGLLGICLILQILTGLFLAMHYTSDTT 60

Query: 61 TAFSSVAHICRDVNYGWIIRYLHANGASMMFFICLYIHVGRGLYGSYTFSETWNVGMVLL 120
          TAFSSVAHICRDVNYGWIIRYLHANGASMMFFICL+IHVGRGLYGSY F ETWN+G++LL
Sbjct: 61 TAFSSVAHICRDVNYGWIIRYLHANGASMMFFICLFIHVGRGLYGSYMFLETWNVIGVILL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180
          FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGT LVEWIWGGFSVDKATLTRFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTDLVEWIWGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLMLLALL 240
          FHFILPFIITAL AVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGAL +ML LL
Sbjct: 181 FHFILPFIITALAAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALFMMLILL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
          ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALV SILI
Sbjct: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVASILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360
          L +P LHTSKQSRM FRP+SQCLFW+LVADL+TLTWIGGQPVE PFI+IGQ+ASILYF
Sbjct: 301 LILMLPLHTSKQRSMMFRPLSQCLFWMLVADLLTLTWIGGQPVEHPFIIIGQLASILYFL 360

Query: 361 LILILMPVAGIENRILKW 379
          +IL+LMP+ ILEN +LKW
Sbjct: 361 IILVLMPIITSIIENLLKW 379

```

tr Q9TGH5 Cytochrome b [cytb] [Tragelaphus strepsiceros (Greater kudu)] 379 AA
Q9TGH5_TRAST align

Score = 723 bits (1866), Expect = 0.0
Identities = 339/379 (89%), Positives = 365/379 (96%)

```

Query: 1 MTNIRKSHPLKIMNDAFIDLPAISNISSWVNFSGLLGVCLIMQILTGLFLAMHYTSDTT 60
          MTNIRKSHPL+KI+N+AFIDLPAISNISSWVNFSGLLG+CLI+QILTGLFLAMHYTSDTT
Sbjct: 1 MTNIRKSHPLMKIVNDAFIDLPAISNISSWVNFSGLLGICLILQILTGLFLAMHYTSDTT 60

Query: 61 TAFSSVAHICRDVNYGWIIRYLHANGASMMFFICLYIHVGRGLYGSYTFSETWNVGMVLL 120
          TAFSSV HICRDVNYGWIIRY+HANGASMMFFICLY+HVGRG+YYSYTF ETWN+G++LL
Sbjct: 61 TAFSSVTHICRDVNYGWIIRYMHANGASMMFFICLYHVHGRGMYYSYTFLETWNVIGVILL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180
          FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGT LVEWIWGGFSVDKATLTRFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTNLVEWIWGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLMLLALL 240
          FHFILPFII AL VHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALL+LAL+
Sbjct: 181 FHFILPFIIAALAMVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLVLALM 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
          +LVLF+PDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI

```

Sbjct: 241 LLVLFPTDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQVPEPPFIMIGQVASILYFS 360
L F+P LHTSKQSRM FRP+SQCLFW+LVADLLTLTWIGGQVPE P+++IGQ+ASI+YF

Sbjct: 301 LIFLPLHTSKQRSMMFRPLSQCLFWILVADLLTLTWIGGQVPEHPYMIIGQLASIMYFL 360

Query: 361 LILILMPVAGIENRILKW 379
LIL+LMPV +IEN +LKW

Sbjct: 361 LILVLMPTSMIENNLKW 379

tr Q5MG70 Cytochrome b [CYTB] [Sus scrofa coreanus] 379 AA
Q5MG70_PIG align

Score = 722 bits (1863), Expect = 0.0
Identities = 343/379 (90%), Positives = 362/379 (95%)

Query: 1 MTNIRKSHPLKIMNDAFIDLPAISNISSWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
MTNIRKSHPL+KI+N+AFIDLPAISNISSWNFGSLLG+CLI+QILTGLFLAMHYTSDTT

Sbjct: 1 MTNIRKSHPLMKIINNAFIDLPAISNISSWNFGSLLGICILQILTGLFLAMHYTSDTT 60

Query: 61 TAFSSVAHICRDVNYGWIIRYLHANGASMFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
TAFSSV HICRDVNYGWIIRYLHANGASMFICL+IHVGRGLYYGSY F ETWN+G+VLL

Sbjct: 61 TAFSSVTHICRDVNYGWIIRYLHANGASMFICLFIHVGRGLYYGSYMFLETWNVGMVLL 120

Query: 121 FTMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSDKATLTRFFA 180
FTMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGT LVEWIWGGFSDKATLTRFFA

Sbjct: 121 FTMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTDLVEWIWGGFSDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLMLLALL 240
FHFILPFIITAL AVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGAL +ML LL

Sbjct: 181 FHFILPFIITALAAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALFMMILLL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALV SILI

Sbjct: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVASILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQVPEPPFIMIGQVASILYFS 360
L +P LHTSKQSRM FRP+SQCLFW+LVADL+TLTWIGGQVPE PFI+IGQ+ASILYF

Sbjct: 301 LILMPLHTSKQRSMMFRPLSQCLFWMLVADLITLTWIGGQVPEHPFIIIGQLASILYFL 360

Query: 361 LILILMPVAGIENRILKW 379
+IL+LMP+ IEN +LKW

Sbjct: 361 IILVLMPTSMIENNLKW 379

tr Q079P0 Cytochrome b [CYTB] [Sus scrofa (Pig)] 379 AA
Q079P0_PIG align

Score = 722 bits (1863), Expect = 0.0
Identities = 343/379 (90%), Positives = 362/379 (95%)

Query: 1 MTNIRKSHPLKIMNDAFIDLPAISNISSWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
MTNIRKSHPL+KI+N+AFIDLPAISNISSWNFGSLLG+CLI+QILTGLFLAMHYTSDTT

Sbjct: 1 MTNIRKSHPLMKIINNAFIDLPAISNISSWNFGSLLGICILQILTGLFLAMHYTSDTT 60

Query: 61 TAFSSVAHICRDVNYGWIIRYLHANGASMFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
TAFSSV HICRDVNYGWIIRYLHANGASMFICL+IHVGRGLYYGSY F ETWN+G+VLL

Sbjct: 61 TAFSSVTHICRDVNYGWIIRYLHANGASMFICLFIHVGRGLYYGSYMFLETWNVGMVLL 120

Query: 121 FTMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSDKATLTRFFA 180
FTMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGT LVEWIWGGFSDKATLTRFFA

Sbjct: 121 FTMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTDLVEWIWGGFSDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLMLLALL 240
FHFILPFIITAL AVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGAL +ML LL

Sbjct: 181 FHFILPFIITALAAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALFMMILLL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALV SILI

Sbjct: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVASILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQVPEPPFIMIGQVASILYFS 360
L +P LHTSKQSRM FRP+SQCLFW+LVADL+TLTWIGGQVPE PFI+IGQ+ASILYF

Sbjct: 301 LILMPLHTSKQRSMMFRPLSQCLFWMLVADLITLTWIGGQVPEHPFIIIGQLASILYFL 360

Query: 361 LILILMPVAGIENRILKW 379
+IL+LMP+ IEN +LKW

Sbjct: 361 IILVLMPTSMIENNLKW 379

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NCBI BLAST program reference [PMID:9254694]:
Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

Query: 141 AA
Date run: 2007-02-09 18:37:24 UTC+0100 on blast01.vital-it.ch
Program: NCBI BLASTP 2.2.15 [Oct-15-2006]
Database: UniProtKB Mammalia
240,475 sequences; 91,865,493 total letters
UniProt Knowledgebase Release 9.6 consists of:
UniProtKB/Swiss-Prot Release 51.6 of 06-Feb-2007: 257964 entries
UniProtKB/TrEMBL Release 34.6 of 06-Feb-2007: 3745801 entries

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List of potentially matching sequences

Send selected sequences to ☐ Include query sequence


Db	AC	Description	Score	E-value
<input type="checkbox"/>	sp P63106	HBA_CAMDR Hemoglobin subunit alpha (Hemoglobin alpha c...	286	2e-77
<input type="checkbox"/>	sp P63105	HBA_CAMBA Hemoglobin subunit alpha (Hemoglobin alpha c...	286	2e-77
<input type="checkbox"/>	sp P67816	HBA_LAMPA Hemoglobin subunit alpha (Hemoglobin alpha c...	281	5e-76
<input type="checkbox"/>	sp P67815	HBA_LAMGU Hemoglobin subunit alpha (Hemoglobin alpha c...	281	5e-76
<input type="checkbox"/>	sp P07425	HBA_LAMVI Hemoglobin subunit alpha (Hemoglobin alpha c...	280	1e-75
<input type="checkbox"/>	sp P01973	HBA_LAMGL Hemoglobin subunit alpha (Hemoglobin alpha c...	278	5e-75
<input type="checkbox"/>	sp P01930	HBA_COLBA Hemoglobin subunit alpha (Hemoglobin alpha c...	254	6e-68
<input type="checkbox"/>	sp P01938	HBA_LORTA Hemoglobin subunit alpha (Hemoglobin alpha c...	254	8e-68
<input type="checkbox"/>	sp P19015	HBA_HIPAM Hemoglobin subunit alpha (Hemoglobin alpha c...	253	2e-67
<input type="checkbox"/>	sp P01928	HBA_CEBAP Hemoglobin subunit alpha (Hemoglobin alpha c...	253	2e-67
<input type="checkbox"/>	sp P01962	HBA_TAPTE Hemoglobin subunit alpha-1/2 (Hemoglobin alp...	251	4e-67
<input type="checkbox"/>	sp P67818	HBA_SAGOE Hemoglobin subunit alpha (Hemoglobin alpha c...	251	7e-67
<input type="checkbox"/>	sp P67817	HBA_ATEGE Hemoglobin subunit alpha (Hemoglobin alpha c...	251	7e-67
<input type="checkbox"/>	sp P01942	HBA_MOUSE Hemoglobin subunit alpha (Hemoglobin alpha c...	250	9e-67
<input type="checkbox"/>	tr Q91VB8	_MOUSE 13 days embryo liver cDNA, RIKEN full-length enr...	250	9e-67
<input type="checkbox"/>	sp P01963	HBA_CERSI Hemoglobin subunit alpha (Hemoglobin alpha c...	249	2e-66
<input type="checkbox"/>	tr Q9CY06	_MOUSE 13 days embryo liver cDNA, RIKEN full-length enr...	249	2e-66
<input type="checkbox"/>	tr Q8BPF4	_MOUSE 11 days embryo whole body cDNA, RIKEN full-lengt...	249	2e-66
<input type="checkbox"/>	sp P07421	HBA_CEBCA Hemoglobin subunit alpha (Hemoglobin alpha c...	249	2e-66
<input type="checkbox"/>	sp P01937	HBA_NYCCO Hemoglobin subunit alpha (Hemoglobin alpha c...	249	3e-66
<input type="checkbox"/>	sp P20854	HBA_CTEGU Hemoglobin subunit alpha (Hemoglobin alpha c...	248	3e-66
<input type="checkbox"/>	sp Q9TS35	HBA1_HYLLA Hemoglobin subunit alpha-1 (Hemoglobin alph...	248	3e-66
<input type="checkbox"/>	sp P19002	HBA_MACNE Hemoglobin subunit alpha-1/2/3 (Hemoglobin a...	248	4e-66
<input type="checkbox"/>	sp P09906	HBA_RHIUN Hemoglobin subunit alpha (Hemoglobin alpha c...	248	6e-66
<input type="checkbox"/>	sp P01965	HBA_PIG Hemoglobin subunit alpha (Hemoglobin alpha cha...	248	6e-66
<input type="checkbox"/>	sp P01958	HBA_HORSE Hemoglobin subunit alpha (Hemoglobin alpha c...	248	6e-66
<input type="checkbox"/>	sp P01945	HBA_MESAU Hemoglobin subunit alpha (Hemoglobin alpha c...	247	8e-66
<input type="checkbox"/>	tr Q1HDT5	_HUMAN Hemoglobin alpha 1-2 hybrid [HBA1] [Homo sapiens...	247	8e-66
<input type="checkbox"/>	sp P21767	HBA_MACFA Hemoglobin subunit alpha-A/Q/R/T (Hemoglobin...	247	1e-65
<input type="checkbox"/>	sp P18972	HBA_CALAR Hemoglobin subunit alpha (Hemoglobin alpha c...	247	1e-65
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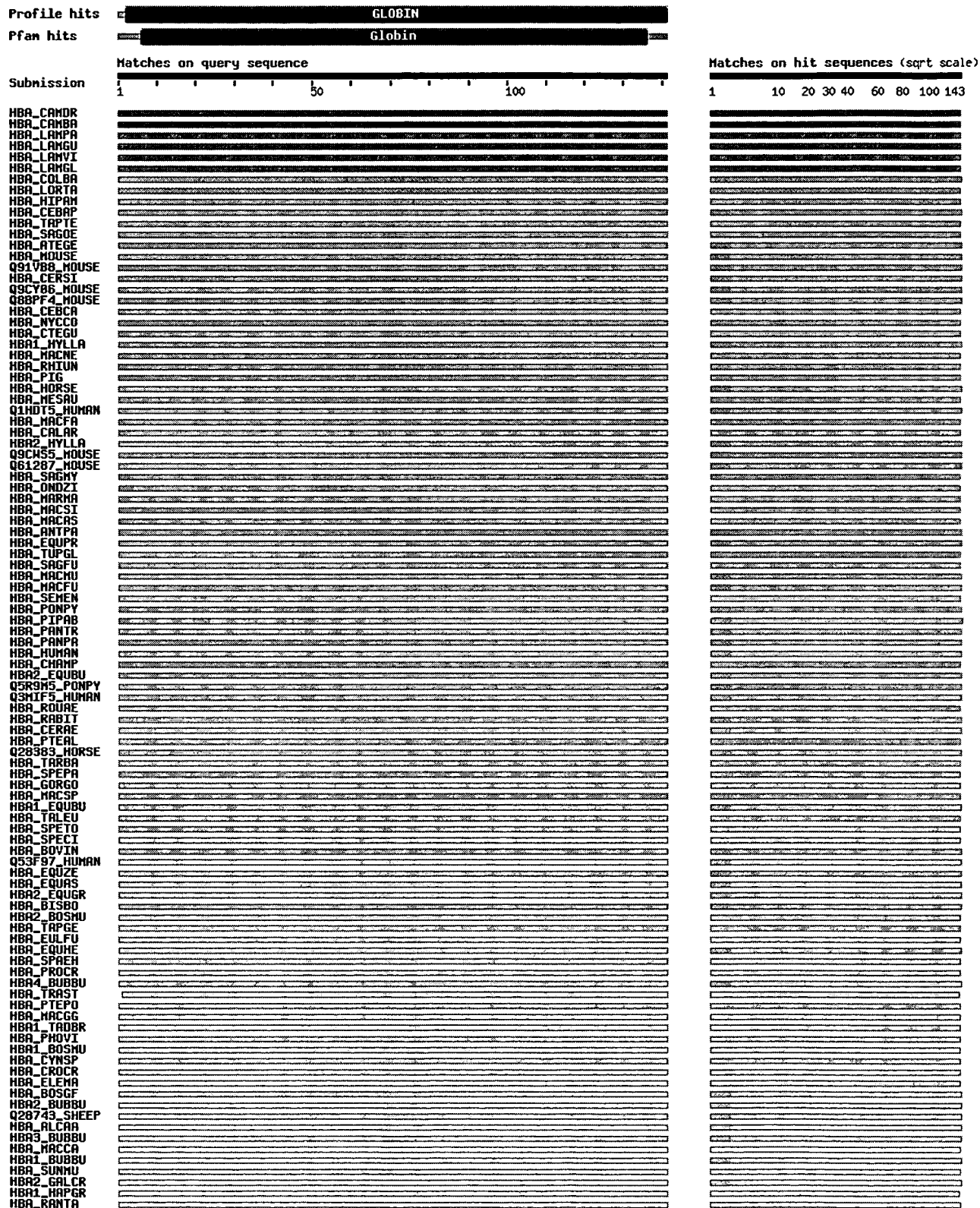

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|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| tr | Q9CWS5 | _MOUSE ES cells cDNA, RIKEN full-length enriched librar... | 247 | 1e-65 |
| tr | Q61287 | _MOUSE Alpha-globin [Hba-al] [Mus musculus (Mouse)] | 247 | 1e-65 |
| sp | Q7M3B6 | HBA_SAGMY Hemoglobin subunit alpha (Hemoglobin alpha c... | 246 | 1e-65 |
| sp | P01944 | HBA_ONDZI Hemoglobin subunit alpha (Hemoglobin alpha c... | 246 | 1e-65 |
| sp | P08852 | HBA_MARMA Hemoglobin subunit alpha (Hemoglobin alpha c... | 246 | 1e-65 |
| sp | P21768 | HBA_MACSI Hemoglobin subunit alpha-1/2 (Hemoglobin alp... | 246 | 1e-65 |
| sp | P21766 | HBA_MACAS Hemoglobin subunit alpha-1/2/3 (Hemoglobin a... | 246 | 1e-65 |
| sp | P14387 | HBA_ANTPA Hemoglobin subunit alpha (Hemoglobin alpha c... | 246 | 1e-65 |
| sp | Q9XSE9 | HBA_EQUPR Hemoglobin subunit alpha (Hemoglobin alpha c... | 246 | 2e-65 |
| sp | P01941 | HBA_TUPGL Hemoglobin subunit alpha (Hemoglobin alpha c... | 246 | 2e-65 |
| sp | P01929 | HBA_SAGFU Hemoglobin subunit alpha (Hemoglobin alpha c... | 246 | 2e-65 |
| sp | P63108 | HBA_MACMU Hemoglobin subunit alpha (Hemoglobin alpha c... | 246 | 2e-65 |
| sp | P63107 | HBA_MACFU Hemoglobin subunit alpha (Hemoglobin alpha c... | 246 | 2e-65 |
| sp | P01924 | HBA_SEMEN Hemoglobin subunit alpha (Hemoglobin alpha c... | 245 | 3e-65 |
| sp | P06635 | HBA_PONPY Hemoglobin subunit alpha (Hemoglobin alpha c... | 245 | 3e-65 |
| sp | Q862A7 | HBA_PIPAB Hemoglobin subunit alpha (Hemoglobin alpha c... | 245 | 3e-65 |
| sp | P69907 | HBA_PANTR Hemoglobin subunit alpha (Hemoglobin alpha c... | 245 | 3e-65 |
| sp | P69906 | HBA_PANPA Hemoglobin subunit alpha (Hemoglobin alpha c... | 245 | 3e-65 |
| sp | P69905 | HBA_HUMAN Hemoglobin subunit alpha (Hemoglobin alpha c... | 245 | 3e-65 |
| sp | Q7M2Y4 | HBA_CHAMP Hemoglobin subunit alpha (Hemoglobin alpha c... | 245 | 3e-65 |
| sp | Q9TVA3 | HBA2_EQUBU Hemoglobin subunit alpha-2 (Hemoglobin alph... | 245 | 3e-65 |
| tr | Q5R9M5 | _PONPY Hypothetical protein DKFZp468J1717 [DKFZp468J171... | 245 | 3e-65 |
| tr | Q3MIF5 | _HUMAN Hemoglobin, alpha 1 (HCG1745306, isoform CRA_b) ... | 245 | 3e-65 |
| sp | P01956 | HBA_ROUAE Hemoglobin subunit alpha (Hemoglobin alpha c... | 245 | 4e-65 |
| sp | P01948 | HBA_RABIT Hemoglobin subunit alpha-1/2 (Hemoglobin alp... | 245 | 4e-65 |
| sp | P01926 | HBA_CERAE Hemoglobin subunit alpha (Hemoglobin alpha c... | 245 | 4e-65 |
| sp | P14389 | HBA_PTEAL Hemoglobin subunit alpha (Hemoglobin alpha c... | 244 | 5e-65 |
| tr | Q28383 | _HORSE Horse BII alpha-2 globin [Equus caballus (Horse)] | 244 | 5e-65 |
| sp | P01940 | HBA_TARBA Hemoglobin subunit alpha (Hemoglobin alpha c... | 244 | 6e-65 |
| sp | P11750 | HBA_SPEPA Hemoglobin subunit alpha (Hemoglobin alpha c... | 244 | 6e-65 |
| sp | P01923 | HBA_GORGO Hemoglobin subunit alpha (Hemoglobin alpha c... | 244 | 6e-65 |
| sp | P07402 | HBA_MACSP Hemoglobin subunit alpha-1/2 (Hemoglobin alp... | 244 | 8e-65 |
| sp | Q9XSN3 | HBA1_EQUBU Hemoglobin subunit alpha-1 (Hemoglobin alph... | 244 | 8e-65 |
| sp | P01951 | HBA_TALEU Hemoglobin subunit alpha (Hemoglobin alpha c... | 243 | 1e-64 |
| sp | P07403 | HBA_SPETO Hemoglobin subunit alpha (Hemoglobin alpha c... | 243 | 1e-64 |
| sp | P09420 | HBA_SPECI Hemoglobin subunit alpha (Hemoglobin alpha c... | 243 | 1e-64 |
| sp | P01966 | HBA_BOVIN Hemoglobin subunit alpha (Hemoglobin alpha c... | 243 | 1e-64 |
| tr | Q53F97 | _HUMAN Alpha 2 globin variant (Fragment) [HBA1] [Homo s... | 243 | 1e-64 |
| sp | P01960 | HBA_EQUZE Hemoglobin subunit alpha (Hemoglobin alpha c... | 243 | 1e-64 |
| sp | P01959 | HBA_EQUAS Hemoglobin subunit alpha (Hemoglobin alpha c... | 243 | 1e-64 |
| sp | Q7JFN6 | HBA2_EQUGR Hemoglobin subunit alpha-2 (Hemoglobin alph... | 243 | 1e-64 |
| sp | P09423 | HBA_BISBO Hemoglobin subunit alpha-I/II (Hemoglobin al... | 242 | 2e-64 |
| sp | P01968 | HBA2_BOSMU Hemoglobin subunit alpha-2 (Hemoglobin alph... | 242 | 2e-64 |
| sp | P28780 | HBA_TAPGE Hemoglobin subunit alpha (Hemoglobin alpha c... | 242 | 3e-64 |
| sp | P01936 | HBA_EULFU Hemoglobin subunit alpha (Hemoglobin alpha c... | 242 | 3e-64 |
| sp | P01961 | HBA_EQUHE Hemoglobin subunit alpha-1/2 (Hemoglobin alp... | 242 | 3e-64 |
| sp | P01943 | HBA_SPAEH Hemoglobin subunit alpha (Hemoglobin alpha c... | 241 | 4e-64 |
| sp | P23019 | HBA_PROCR Hemoglobin subunit alpha (Hemoglobin alpha c... | 241 | 4e-64 |
| sp | Q9XSK1 | HBA4_BUBBU Hemoglobin subunit alpha-4 (Hemoglobin alph... | 241 | 4e-64 |
| sp | P04237 | HBA_TRAST Hemoglobin subunit alpha (Hemoglobin alpha c... | 241 | 5e-64 |
| sp | P14390 | HBA_PTEPO Hemoglobin subunit alpha (Hemoglobin alpha c... | 241 | 7e-64 |
| sp | P24659 | HBA_MACGG Hemoglobin subunit alpha-1/2 (Hemoglobin alp... | 241 | 7e-64 |
| sp | P11755 | HBA1_TADBR Hemoglobin subunit alpha-1 (Hemoglobin alph... | 241 | 7e-64 |
| sp | P09908 | HBA_PHOVI Hemoglobin subunit alpha (Hemoglobin alpha c... | 240 | 9e-64 |
| sp | P01967 | HBA1_BOSMU Hemoglobin subunit alpha-1 (Hemoglobin alph... | 240 | 9e-64 |
| sp | P11753 | HBA_CYNBP Hemoglobin subunit alpha (Hemoglobin alpha c... | 240 | 1e-63 |
| sp | P18973 | HBA_CROCR Hemoglobin subunit alpha (Hemoglobin alpha c... | 240 | 1e-63 |
| sp | P01954 | HBA_ELEMA Hemoglobin subunit alpha (Hemoglobin alpha c... | 239 | 2e-63 |
| sp | P01969 | HBA_BOSGF Hemoglobin subunit alpha (Hemoglobin alpha c... | 239 | 2e-63 |
| sp | Q9TSN8 | HBA2_BUBBU Hemoglobin subunit alpha-2 (Hemoglobin alph... | 239 | 2e-63 |
| tr | Q28743 | _SHEEP Alpha globin chain [Ovis aries (Sheep)] | 239 | 2e-63 |
| sp | P01971 | HBA_ALCAA Hemoglobin subunit alpha (Hemoglobin alpha c... | 239 | 2e-63 |
| sp | Q9TSN9 | HBA3_BUBBU Hemoglobin subunit alpha-3 (Hemoglobin alph... | 239 | 2e-63 |
| sp | P09839 | HBA_MACCA Hemoglobin subunit alpha (Hemoglobin alpha c... | 239 | 3e-63 |
| sp | Q9TSN7 | HBA1_BUBBU Hemoglobin subunit alpha-1 (Hemoglobin alph... | 239 | 3e-63 |
| sp | P01950 | HBA_SUNMU Hemoglobin subunit alpha (Hemoglobin alpha c... | 238 | 3e-63 |

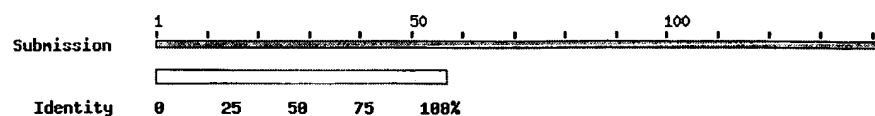
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☐ sp P01939 HBA2_GALCR Hemoglobin subunit alpha-B (Hemoglobin alph... 238 3e-63
☐ sp Q7M3B8 HBA1_HAPGR Hemoglobin subunit alpha-1 (Hemoglobin alph... 238 3e-63
☐ sp P21379 HBA_RANTA Hemoglobin subunit alpha (Hemoglobin alpha c... 238 5e-63

Graphical overview of the alignments

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( Help) (use ScanProsite for more details about PROSITE matches)





Alignments

sp P63106 Hemoglobin subunit alpha (Hemoglobin alpha chain) (Alpha-globin) 141 AA
HBA_CAMDR [HBA] [Camelus dromedarius (Dromedary) (Arabian camel)] align

Score = 286 bits (731), Expect = 2e-77
Identities = 141/141 (100%), Positives = 141/141 (100%)

Query: 1 VLSSKDKTNVKTAFGKIGGHAAEYGAEALERMFLGFPTTKTYFPHFDLSHGSAQVKAHGK 60
VLSSKDKTNVKTAFGKIGGHAAEYGAEALERMFLGFPTTKTYFPHFDLSHGSAQVKAHGK
Sbjct: 1 VLSSKDKTNVKTAFGKIGGHAAEYGAEALERMFLGFPTTKTYFPHFDLSHGSAQVKAHGK 60

Query: 61 KVGDALTKAADHLDDLPSALSALSDLHAHKL RVD PVNFKLLSHCLLVTVAAHHPGDFTPS 120
KVGDALTKAADHLDDLPSALSALSDLHAHKL RVD PVNFKLLSHCLLVTVAAHHPGDFTPS
Sbjct: 61 KVGDALTKAADHLDDLPSALSALSDLHAHKL RVD PVNFKLLSHCLLVTVAAHHPGDFTPS 120

Query: 121 VHASLDKFLANVSTVLTSKYR 141
VHASLDKFLANVSTVLTSKYR
Sbjct: 121 VHASLDKFLANVSTVLTSKYR 141

sp P63105 Hemoglobin subunit alpha (Hemoglobin alpha chain) (Alpha-globin) 141 AA
HBA_CAMBA [HBA] [Camelus bactrianus (Bactrian camel)] align

Score = 286 bits (731), Expect = 2e-77
Identities = 141/141 (100%), Positives = 141/141 (100%)

Query: 1 VLSSKDKTNVKTAFGKIGGHAAEYGAEALERMFLGFPTTKTYFPHFDLSHGSAQVKAHGK 60
VLSSKDKTNVKTAFGKIGGHAAEYGAEALERMFLGFPTTKTYFPHFDLSHGSAQVKAHGK
Sbjct: 1 VLSSKDKTNVKTAFGKIGGHAAEYGAEALERMFLGFPTTKTYFPHFDLSHGSAQVKAHGK 60

Query: 61 KVGDALTKAADHLDDLPSALSALSDLHAHKL RVD PVNFKLLSHCLLVTVAAHHPGDFTPS 120
KVGDALTKAADHLDDLPSALSALSDLHAHKL RVD PVNFKLLSHCLLVTVAAHHPGDFTPS
Sbjct: 61 KVGDALTKAADHLDDLPSALSALSDLHAHKL RVD PVNFKLLSHCLLVTVAAHHPGDFTPS 120

Query: 121 VHASLDKFLANVSTVLTSKYR 141
VHASLDKFLANVSTVLTSKYR
Sbjct: 121 VHASLDKFLANVSTVLTSKYR 141

sp P67816 Hemoglobin subunit alpha (Hemoglobin alpha chain) (Alpha-globin) 141 AA
HBA_LAMPA [HBA] [Lama guanicoe pacos (Alpaca) (Lama pacos)] align

Score = 281 bits (719), Expect = 5e-76
Identities = 137/141 (97%), Positives = 140/141 (99%)

Query: 1 VLSSKDKTNVKTAFGKIGGHAAEYGAEALERMFLGFPTTKTYFPHFDLSHGSAQVKAHGK 60
VLSSKDK N+KTAFGKIGGHAA+YGAEALERMFLGFPTTKTYFPHFDLSHGSAQVKAHGK
Sbjct: 1 VLSSKDKANIKTAFGKIGGHAAEYGAEALERMFLGFPTTKTYFPHFDLSHGSAQVKAHGK 60

Query: 61 KVGDALTKAADHLDDLPSALSALSDLHAHKL RVD PVNFKLLSHCLLVTVAAHHPGDFTPS 120
KVGDALTKAADHLDDLPSALSALSDLHAHKL RVD PVNFKLLSHCLLVTVAAHHPGDFTPS+
Sbjct: 61 KVGDALTKAADHLDDLPSALSALSDLHAHKL RVD PVNFKLLSHCLLVTVAAHHPGDFTPA 120

Query: 121 VHASLDKFLANVSTVLTSKYR 141
VHASLDKFLANVSTVLTSKYR
Sbjct: 121 VHASLDKFLANVSTVLTSKYR 141

sp P67815 Hemoglobin subunit alpha (Hemoglobin alpha chain) (Alpha-globin) 141 AA
HBA_LAMGU [HBA] [Lama guanicoe (Guanaco)] align

Score = 281 bits (719), Expect = 5e-76
Identities = 137/141 (97%), Positives = 140/141 (99%)

```
Query: 1  VLSSKDKTNVKTAFGKIGGHAAEYGAEALERMFLGFPTTKTYFPHFDLSHGSAQVKAHGK 60
          VLSSKDK N+KTAFGKIGGHAA+YGAEALERMFLGFPTTKTYFPHFDLSHGSAQVKAHGK
Sbjct: 1  VLSSKDKANIKTAFGKIGGHAAEYGAEALERMFLGFPTTKTYFPHFDLSHGSAQVKAHGK 60

Query: 61  KVGDAITKAADHLDDLPSALSALSDLHAHKLKRVDPVNFKLLSHCLLVTVAAHHPGDFTPS 120
          KVGDAITKAADHLDDLPSALSALSDLHAHKLKRVDPVNFKLLSHCLLVTVAAHHPGDFTP+
Sbjct: 61  KVGDAITKAADHLDDLPSALSALSDLHAHKLKRVDPVNFKLLSHCLLVTVAAHHPGDFTPA 120

Query: 121 VHASLDKFLANVSTVLTSKYR 141
          VHASLDKFLANVSTVLTSKYR
Sbjct: 121 VHASLDKFLANVSTVLTSKYR 141
```

sp P07425 Hemoglobin subunit alpha (Hemoglobin alpha chain) (Alpha-globin) 141 AA
HBA_LAMVI [HBA] [Lama vicugna (Vicugna) (Vicugna vicugna)] align

Score = 280 bits (716), Expect = 1e-75
Identities = 137/141 (97%), Positives = 139/141 (98%)

```
Query: 1  VLSSKDKTNVKTAFGKIGGHAAEYGAEALERMFLGFPTTKTYFPHFDLSHGSAQVKAHGK 60
          VLSSKDK NVKTAFGKIGGHAA+YGAEALERMFLGFPTTKTYFPHFDLSHGSAQVKAHGK
Sbjct: 1  VLSSKDKANVKTAFGKIGGHAAEYGAEALERMFLGFPTTKTYFPHFDLSHGSAQVKAHGK 60

Query: 61  KVGDAITKAADHLDDLPSALSALSDLHAHKLKRVDPVNFKLLSHCLLVTVAAHHPGDFTPS 120
          KVGDAITKAADHLDDLPSALSALSDLHAHKLKRVDPVNFKLLSHCLLVTVAAHHPGDFTP+
Sbjct: 61  KVGDAITKAADHLDDLPSALSALSDLHAHKLKRVDPVNFKLLSHCLLVTVAAHHPGDFTPA 120

Query: 121 VHASLDKFLANVSTVLTSKYR 141
          VHASLDKFL NVSTVLTSKYR
Sbjct: 121 VHASLDKFLTNVSTVLTSKYR 141
```

sp P01973 Hemoglobin subunit alpha (Hemoglobin alpha chain) (Alpha-globin) 141 AA
HBA_LAMGL [HBA] [Lama glama (Llama)] align

Score = 278 bits (710), Expect = 5e-75
Identities = 136/141 (96%), Positives = 139/141 (98%)

```
Query: 1  VLSSKDKTNVKTAFGKIGGHAAEYGAEALERMFLGFPTTKTYFPHFDLSHGSAQVKAHGK 60
          VLSSKDK N+KTAFGKIGGHAA+YGAEALERMFLGFPTTKTYFPHFDLSHGSAQVKAHGK
Sbjct: 1  VLSSKDKANIKTAFGKIGGHAAEYGAEALERMFLGFPTTKTYFPHFDLSHGSAQVKAHGK 60

Query: 61  KVGDAITKAADHLDDLPSALSALSDLHAHKLKRVDPVNFKLLSHCLLVTVAAHHPGDFTPS 120
          KVGDAITKAADHLDDLPSALSALSDLHAHKLKRVDPVNFKLLSHCLLVTVAAHHPGDFTP+
Sbjct: 61  KVGDAITKAADHLDDLPSALSALSDLHAHKLKRVDPVNFKLLSHCLLVTVAAHHPGDFTPA 120

Query: 121 VHASLDKFLANVSTVLTSKYR 141
          V ASLDKFLANVSTVLTSKYR
Sbjct: 121 VDASLDKFLANVSTVLTSKYR 141
```

sp P01930 Hemoglobin subunit alpha (Hemoglobin alpha chain) (Alpha-globin) 142 AA
HBA_COLBA [HBA] [Colobus badius (Red colobus) (Procolobus badius)] align

Score = 254 bits (649), Expect = 6e-68
Identities = 123/141 (87%), Positives = 131/141 (92%)

```
Query: 1  VLSSKDKTNVKTAFGKIGGHAAEYGAEALERMFLGFPTTKTYFPHFDLSHGSAQVKAHGK 60
          VLS DKTNVKTA+GK+GGH EYGAEALERMFL FPTTKTYFPHFDLSHGSAQVK HGK
Sbjct: 2  VLSPADKTNVKTAWKVGGHGGEYGAEALERMFLSFPTTKTYFPHFDLSHGSAQVKHGK 61

Query: 61  KVGDAITKAADHLDDLPSALSALSDLHAHKLKRVDPVNFKLLSHCLLVTVAAHHPGDFTPS 120
          KV DALT AA H+DD+PSALSALSDLHAHKLKRVDPVNFKLLSHCLLVTVAAHHP +FTP+
Sbjct: 62  KVADALTAAAHVDDMPALSALSDLHAHKLKRVDPVNFKLLSHCLLVTLAAHHPAEFTPA 121

Query: 121 VHASLDKFLANVSTVLTSKYR 141
          VHASLDKFLA+VSTVLTSKYR
Sbjct: 122 VHASLDKFLASVSTVLTSKYR 142
```

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If your question is not covered, please contact <helpdesk@expasy.org>.

NCBI BLAST program reference [PMID:9254694]:
Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

Query: 147 AA
Date run: 2007-02-09 18:42:06 UTC+0100 on blast01.vital-it.ch
Program: NCBI BLASTP 2.2.15 [Oct-15-2006]
Database: UniProtKB Mammalia
240,475 sequences; 91,865,493 total letters
UniProt Knowledgebase Release 9.6 consists of:
UniProtKB/Swiss-Prot Release 51.6 of 06-Feb-2007: 257964 entries
UniProtKB/TrEMBL Release 34.6 of 06-Feb-2007: 3745801 entries

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List of potentially matching sequences

Send selected sequences to ☐ Include query sequence

Db	AC	Description	Score	E-value
<input type="checkbox"/>	sp P68231	HBB_CAMDR Hemoglobin subunit beta (Hemoglobin beta cha...	303	2e-82
<input type="checkbox"/>	sp P68230	HBB_CAMBA Hemoglobin subunit beta (Hemoglobin beta cha...	303	2e-82
<input type="checkbox"/>	sp P68227	HBB_LAMVI Hemoglobin subunit beta (Hemoglobin beta cha...	298	4e-81
<input type="checkbox"/>	sp P68228	HBB_LAMPA Hemoglobin subunit beta (Hemoglobin beta cha...	298	4e-81
<input type="checkbox"/>	sp P68229	HBB_LAMGU Hemoglobin subunit beta (Hemoglobin beta cha...	298	4e-81
<input type="checkbox"/>	sp P68226	HBB_LAMGL Hemoglobin subunit beta (Hemoglobin beta cha...	298	4e-81
<input type="checkbox"/>	sp P18983	HBB_AILME Hemoglobin subunit beta (Hemoglobin beta cha...	265	4e-71
<input type="checkbox"/>	sp P14391	HBB_PTEAL Hemoglobin subunit beta (Hemoglobin beta cha...	264	7e-71
<input type="checkbox"/>	sp P14392	HBB_PTEPO Hemoglobin subunit beta (Hemoglobin beta cha...	264	9e-71
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<input type="checkbox"/>	sp P68011	HBB_URSMA Hemoglobin subunit beta (Hemoglobin beta cha...	262	3e-70
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<input type="checkbox"/>	sp Q6WN29	HBB_ALOBE Hemoglobin subunit beta (Hemoglobin beta cha...	262	3e-70
<input type="checkbox"/>	sp Q6WN21	HBB_CALGO Hemoglobin subunit beta (Hemoglobin beta cha...	261	6e-70
<input type="checkbox"/>	sp P68232	HBB_ATEGE Hemoglobin subunit beta (Hemoglobin beta cha...	261	6e-70
<input type="checkbox"/>	sp P68234	HBB_ATEBE Hemoglobin subunit beta (Hemoglobin beta cha...	261	6e-70
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<input type="checkbox"/>	sp P09909	HBB_PHOVI Hemoglobin subunit beta (Hemoglobin beta cha...	259	2e-69
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<input type="checkbox"/>	sp Q6WN22	HBB_ATEPA Hemoglobin subunit beta (Hemoglobin beta cha...	259	2e-69
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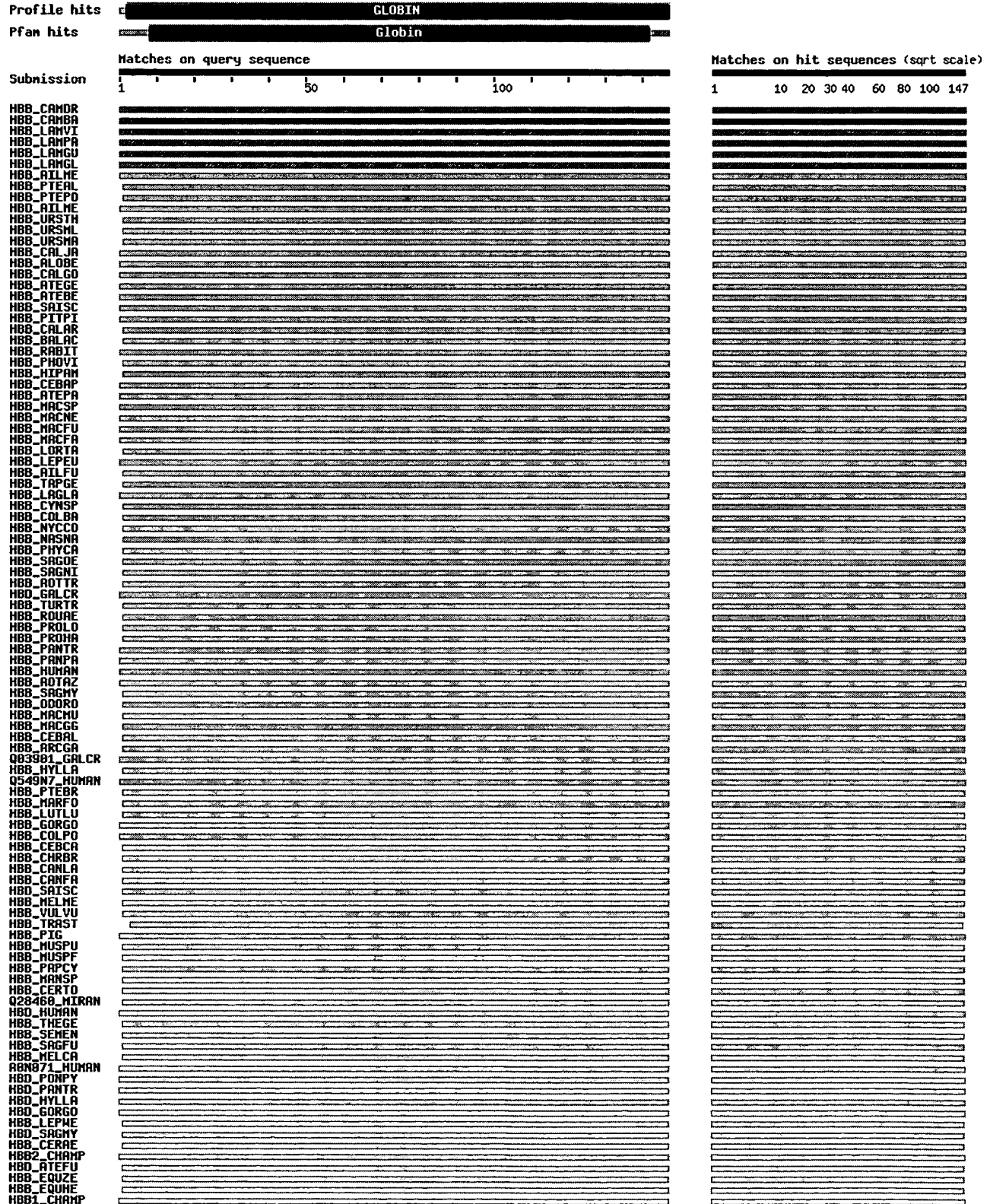
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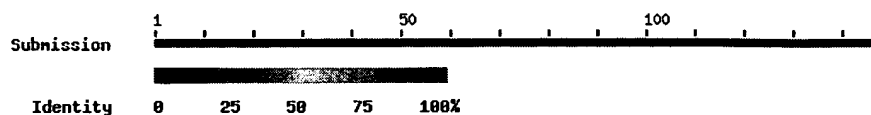
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[ ] sp P08535 HBB_LEPEU Hemoglobin subunit beta (Hemoglobin beta cha... 259 2e-69
[ ] sp P18982 HBB_AILFU Hemoglobin subunit beta (Hemoglobin beta cha... 259 2e-69
[ ] sp P28781 HBB_TAGGE Hemoglobin subunit beta (Hemoglobin beta cha... 259 3e-69
[ ] sp Q6WN25 HBB_LAGLA Hemoglobin subunit beta (Hemoglobin beta cha... 259 3e-69
[ ] sp P11754 HBB_CYNBP Hemoglobin subunit beta (Hemoglobin beta cha... 259 3e-69
[ ] sp P02033 HBB_COLBA Hemoglobin subunit beta (Hemoglobin beta cha... 259 3e-69
[ ] sp P02049 HBB_NYCCO Hemoglobin subunit beta (Hemoglobin beta cha... 258 4e-69
[ ] sp P26916 HBB_NASNA Hemoglobin subunit beta (Hemoglobin beta cha... 258 4e-69
[ ] sp P09905 HBB_PHYCA Hemoglobin subunit beta-1/2 (Hemoglobin beta... 258 5e-69
[ ] sp P68055 HBB_SAGOE Hemoglobin subunit beta (Hemoglobin beta cha... 257 8e-69
[ ] sp P68054 HBB_SAGNI Hemoglobin subunit beta (Hemoglobin beta cha... 257 8e-69
[ ] sp P02035 HBB_AOTTR Hemoglobin subunit beta (Hemoglobin beta cha... 257 8e-69
[ ] sp Q03902 HBD_GALCR Hemoglobin subunit delta (Hemoglobin delta c... 257 1e-68
[ ] sp P18990 HBB_TURTR Hemoglobin subunit beta (Hemoglobin beta cha... 257 1e-68
[ ] sp P02058 HBB_ROUAE Hemoglobin subunit beta (Hemoglobin beta cha... 256 1e-68
[ ] sp P18989 HBB_PROLO Hemoglobin subunit beta (Hemoglobin beta cha... 256 1e-68
[ ] sp P02086 HBB_PROHA Hemoglobin subunit beta (Hemoglobin beta cha... 256 1e-68
[ ] sp P68873 HBB_PANTR Hemoglobin subunit beta (Hemoglobin beta cha... 256 1e-68
[ ] sp P68872 HBB_PANPA Hemoglobin subunit beta (Hemoglobin beta cha... 256 1e-68
[ ] sp P68871 HBB_HUMAN Hemoglobin subunit beta (Hemoglobin beta cha... 256 1e-68
[ ] sp Q6WN26 HBB_AOTAZ Hemoglobin subunit beta (Hemoglobin beta cha... 256 1e-68
[ ] sp P02038 HBB_SAGMY Hemoglobin subunit beta (Hemoglobin beta cha... 256 2e-68
[ ] sp P68046 HBB_ODORO Hemoglobin subunit beta (Hemoglobin beta cha... 256 2e-68
[ ] sp P02026 HBB_MACMU Hemoglobin subunit beta (Hemoglobin beta cha... 256 2e-68
[ ] sp P24660 HBB_MACGG Hemoglobin subunit beta (Hemoglobin beta cha... 256 2e-68
[ ] sp P02040 HBB_CEBAL Hemoglobin subunit beta (Hemoglobin beta cha... 256 2e-68
[ ] sp P68047 HBB_ARCGA Hemoglobin subunit beta (Hemoglobin beta cha... 256 2e-68
[ ] tr Q03901 _GALCR Beta-globin protein [beta-globin] [Galago crassi... 256 2e-68
[ ] sp P02025 HBB_HYLLA Hemoglobin subunit beta (Hemoglobin beta cha... 256 2e-68
[ ] tr Q549N7 _HUMAN Mutant beta-globin [HBB] [Homo sapiens (Human)] 256 2e-68
[ ] sp P68052 HBB_PTEBR Hemoglobin subunit beta (Hemoglobin beta cha... 255 3e-68
[ ] sp P68053 HBB_MARFO Hemoglobin subunit beta (Hemoglobin beta cha... 255 3e-68
[ ] sp P10893 HBB_LUTLU Hemoglobin subunit beta (Hemoglobin beta cha... 255 3e-68
[ ] sp P02024 HBB_GORGO Hemoglobin subunit beta (Hemoglobin beta cha... 255 3e-68
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[ ] sp P67822 HBB_CEBCA Hemoglobin subunit beta (Hemoglobin beta cha... 255 3e-68
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[ ] sp P02047 HBD_SAISC Hemoglobin subunit delta (Hemoglobin delta c... 254 5e-68
[ ] sp P02055 HBB_MELEME Hemoglobin subunit beta (Hemoglobin beta cha... 254 5e-68
[ ] sp P21201 HBB_VULVU Hemoglobin subunit beta (Hemoglobin beta cha... 254 7e-68
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[ ] sp P02030 HBB_PAPCY Hemoglobin subunit beta (Hemoglobin beta cha... 254 9e-68
[ ] sp P08259 HBB_MANSP Hemoglobin subunit beta (Hemoglobin beta cha... 254 9e-68
[ ] sp P02031 HBB_CERTO Hemoglobin subunit beta (Hemoglobin beta cha... 253 1e-67
[ ] tr Q28460 _MIRAN MRNA, . (Fragment) [Mirounga angustirostris (Nor... 253 1e-67
[ ] sp P02042 HBD_HUMAN Hemoglobin subunit delta (Hemoglobin delta c... 253 2e-67
[ ] sp P02029 HBB_THEGE Hemoglobin subunit beta (Hemoglobin beta cha... 253 2e-67
[ ] sp P02032 HBB_SEMEN Hemoglobin subunit beta (Hemoglobin beta cha... 253 2e-67
[ ] sp P02039 HBB_SAGFU Hemoglobin subunit beta (Hemoglobin beta cha... 253 2e-67
[ ] sp P15449 HBB_MELCA Hemoglobin subunit beta (Hemoglobin beta cha... 253 2e-67
[ ] tr A0N071 _HUMAN Delta-globin chain (Hemoglobin delta) [HBD] [Hom... 253 2e-67
[ ] sp P61775 HBD_PONPY Hemoglobin subunit delta (Hemoglobin delta c... 253 2e-67
[ ] sp P61772 HBD_PANTR Hemoglobin subunit delta (Hemoglobin delta c... 253 2e-67
[ ] sp P61774 HBD_HYLLA Hemoglobin subunit delta (Hemoglobin delta c... 253 2e-67
[ ] sp P61773 HBD_GORGO Hemoglobin subunit delta (Hemoglobin delta c... 253 2e-67
[ ] sp P15166 HBB_LEPWE Hemoglobin subunit beta (Hemoglobin beta cha... 252 3e-67
[ ] sp P68014 HBD_SAGMY Hemoglobin subunit delta (Hemoglobin delta c... 252 3e-67
[ ] sp P02028 HBB_CERAE Hemoglobin subunit beta (Hemoglobin beta cha... 252 3e-67
[ ] sp Q7M2Y5 HBB2_CHAMP Hemoglobin subunit beta-2 (Hemoglobin beta-... 251 4e-67
[ ] sp P33499 HBD_ATEFU Hemoglobin subunit delta (Hemoglobin delta c... 251 6e-67
```

- ☐ sp P67824 HBB_EQUZE Hemoglobin subunit beta (Hemoglobin beta cha... 251 6e-67
☐ sp P67823 HBB_EQUHE Hemoglobin subunit beta (Hemoglobin beta cha... 251 6e-67
☐ sp P68087 HBB1_CHAMP Hemoglobin subunit beta-1 (Hemoglobin beta-... 251 6e-67

Graphical overview of the alignments

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Alignments

sp P68231 Hemoglobin subunit beta (Hemoglobin beta chain) (Beta-globin) [HBB] 147 AA
HBB_CAMDR [Camelus dromedarius (Dromedary) (Arabian camel)] align

Score = 303 bits (775), Expect = 2e-82
Identities = 147/147 (100%), Positives = 147/147 (100%)

Query: 1 MVHLSGDEKNAVHGLWSKVQVDEVGGEALGRLLVVYPWTRRRFFESFGDLSTADAVMNNPK 60
MVHLSGDEKNAVHGLWSKVQVDEVGGEALGRLLVVYPWTRRRFFESFGDLSTADAVMNNPK
Sbjct: 1 MVHLSGDEKNAVHGLWSKVQVDEVGGEALGRLLVVYPWTRRRFFESFGDLSTADAVMNNPK 60

Query: 61 VKAHGSKVLNSFGDGLNHLNLDNLKGTAKLSELHCDKLHVDPENFRLLGNVLVVVLARHFG 120
VKAHGSKVLNSFGDGLNHLNLDNLKGTAKLSELHCDKLHVDPENFRLLGNVLVVVLARHFG
Sbjct: 61 VKAHGSKVLNSFGDGLNHLNLDNLKGTAKLSELHCDKLHVDPENFRLLGNVLVVVLARHFG 120

Query: 121 KEFTPDQAAYQKVAVGVANALAHRYH 147
KEFTPDQAAYQKVAVGVANALAHRYH
Sbjct: 121 KEFTPDQAAYQKVAVGVANALAHRYH 147

sp P68230 Hemoglobin subunit beta (Hemoglobin beta chain) (Beta-globin) [HBB] 147 AA
HBB_CAMBA [Camelus bactrianus (Bactrian camel)] align

Score = 303 bits (775), Expect = 2e-82
Identities = 147/147 (100%), Positives = 147/147 (100%)

Query: 1 MVHLSGDEKNAVHGLWSKVQVDEVGGEALGRLLVVYPWTRRRFFESFGDLSTADAVMNNPK 60
MVHLSGDEKNAVHGLWSKVQVDEVGGEALGRLLVVYPWTRRRFFESFGDLSTADAVMNNPK
Sbjct: 1 MVHLSGDEKNAVHGLWSKVQVDEVGGEALGRLLVVYPWTRRRFFESFGDLSTADAVMNNPK 60

Query: 61 VKAHGSKVLNSFGDGLNHLNLDNLKGTAKLSELHCDKLHVDPENFRLLGNVLVVVLARHFG 120
VKAHGSKVLNSFGDGLNHLNLDNLKGTAKLSELHCDKLHVDPENFRLLGNVLVVVLARHFG
Sbjct: 61 VKAHGSKVLNSFGDGLNHLNLDNLKGTAKLSELHCDKLHVDPENFRLLGNVLVVVLARHFG 120

Query: 121 KEFTPDQAAYQKVAVGVANALAHRYH 147
KEFTPDQAAYQKVAVGVANALAHRYH
Sbjct: 121 KEFTPDQAAYQKVAVGVANALAHRYH 147

sp P68227 Hemoglobin subunit beta (Hemoglobin beta chain) (Beta-globin) [HBB] 147 AA
HBB_LAMVI [Lama vicugna (Vicugna) (Vicugna vicugna)] align

Score = 298 bits (763), Expect = 4e-81
Identities = 145/147 (98%), Positives = 147/147 (100%)

Query: 1 MVHLSGDEKNAVHGLWSKVQVDEVGGEALGRLLVVYPWTRRRFFESFGDLSTADAVMNNPK 60
MV+LSGDEKNAVHGLWSKVQVDEVGGEALGRLLVVYPWTRRRFFESFGDLSTADAVMNNPK
Sbjct: 1 MVNLSGDEKNAVHGLWSKVQVDEVGGEALGRLLVVYPWTRRRFFESFGDLSTADAVMNNPK 60

Query: 61 VKAHGSKVLNSFGDGLNHLNLDNLKGTAKLSELHCDKLHVDPENFRLLGNVLVVVLARHFG 120
VKAHGSKVLNSFGDGL+HLNLDNLKGTAKLSELHCDKLHVDPENFRLLGNVLVVVLARHFG
Sbjct: 61 VKAHGSKVLNSFGDGLSHLDNLKGTAKLSELHCDKLHVDPENFRLLGNVLVVVLARHFG 120

Query: 121 KEFTPDQAAYQKVAVGVANALAHRYH 147
KEFTPDQAAYQKVAVGVANALAHRYH
Sbjct: 121 KEFTPDQAAYQKVAVGVANALAHRYH 147

sp P68228 Hemoglobin subunit beta (Hemoglobin beta chain) (Beta-globin) [HBB] 147 AA
HBB_LAMPA [Lama guanicoe pacos (Alpaca) (Lama pacos)] align

Score = 298 bits (763), Expect = 4e-81
Identities = 145/147 (98%), Positives = 147/147 (100%)

```
Query: 1  MVHLSGDEKNAVHGLWSKVVDVGGGALGRLLVVYPWTRRRFFESFGDLSTADAVMNNPK 60
          MV+LSGDEKNAVHGLWSKVVDVGGGALGRLLVVYPWTRRRFFESFGDLSTADAVMNNPK
Sbjct: 1  MVNLSGDEKNAVHGLWSKVVDVGGGALGRLLVVYPWTRRRFFESFGDLSTADAVMNNPK 60

Query: 61  VKAHGSKVLNSFGDGLNHLNLDNLKGTAKLSELHCDKLHVDPENFRLLGNVLVVVLARHFG 120
          VKAHGSKVLNSFGDGL+HLDNLKGTAKLSELHCDKLHVDPENFRLLGNVLVVVLARHFG
Sbjct: 61  VKAHGSKVLNSFGDGLSHLDNLKGTAKLSELHCDKLHVDPENFRLLGNVLVVVLARHFG 120

Query: 121 KEFTPDLQAAYQKVAVGVANALAHRYH 147
          KEFTPDLQAAYQKVAVGVANALAHRYH
Sbjct: 121 KEFTPDLQAAYQKVAVGVANALAHRYH 147
```

sp P68229 Hemoglobin subunit beta (Hemoglobin beta chain) (Beta-globin) [HBB] 147 AA
HBB_LAMGU [Lama guanicoe (Guanaco)] align

Score = 298 bits (763), Expect = 4e-81
Identities = 145/147 (98%), Positives = 147/147 (100%)

```
Query: 1  MVHLSGDEKNAVHGLWSKVVDVGGGALGRLLVVYPWTRRRFFESFGDLSTADAVMNNPK 60
          MV+LSGDEKNAVHGLWSKVVDVGGGALGRLLVVYPWTRRRFFESFGDLSTADAVMNNPK
Sbjct: 1  MVNLSGDEKNAVHGLWSKVVDVGGGALGRLLVVYPWTRRRFFESFGDLSTADAVMNNPK 60

Query: 61  VKAHGSKVLNSFGDGLNHLNLDNLKGTAKLSELHCDKLHVDPENFRLLGNVLVVVLARHFG 120
          VKAHGSKVLNSFGDGL+HLDNLKGTAKLSELHCDKLHVDPENFRLLGNVLVVVLARHFG
Sbjct: 61  VKAHGSKVLNSFGDGLSHLDNLKGTAKLSELHCDKLHVDPENFRLLGNVLVVVLARHFG 120

Query: 121 KEFTPDLQAAYQKVAVGVANALAHRYH 147
          KEFTPDLQAAYQKVAVGVANALAHRYH
Sbjct: 121 KEFTPDLQAAYQKVAVGVANALAHRYH 147
```

sp P68226 Hemoglobin subunit beta (Hemoglobin beta chain) (Beta-globin) [HBB] 147 AA
HBB_LAMGL [Lama glama (Llama)] align

Score = 298 bits (763), Expect = 4e-81
Identities = 145/147 (98%), Positives = 147/147 (100%)

```
Query: 1  MVHLSGDEKNAVHGLWSKVVDVGGGALGRLLVVYPWTRRRFFESFGDLSTADAVMNNPK 60
          MV+LSGDEKNAVHGLWSKVVDVGGGALGRLLVVYPWTRRRFFESFGDLSTADAVMNNPK
Sbjct: 1  MVNLSGDEKNAVHGLWSKVVDVGGGALGRLLVVYPWTRRRFFESFGDLSTADAVMNNPK 60

Query: 61  VKAHGSKVLNSFGDGLNHLNLDNLKGTAKLSELHCDKLHVDPENFRLLGNVLVVVLARHFG 120
          VKAHGSKVLNSFGDGL+HLDNLKGTAKLSELHCDKLHVDPENFRLLGNVLVVVLARHFG
Sbjct: 61  VKAHGSKVLNSFGDGLSHLDNLKGTAKLSELHCDKLHVDPENFRLLGNVLVVVLARHFG 120

Query: 121 KEFTPDLQAAYQKVAVGVANALAHRYH 147
          KEFTPDLQAAYQKVAVGVANALAHRYH
Sbjct: 121 KEFTPDLQAAYQKVAVGVANALAHRYH 147
```

sp P18983 Hemoglobin subunit beta (Hemoglobin beta chain) (Beta-globin) [HBB] 147 AA
HBB_AILME [Ailuropoda melanoleuca (Giant panda)] align

Score = 265 bits (677), Expect = 4e-71
Identities = 127/147 (86%), Positives = 137/147 (93%)

```
Query: 1  MVHLSGDEKNAVHGLWSKVVDVGGGALGRLLVVYPWTRRRFFESFGDLSTADAVMNNPK 60
          MVHL+G+EK AV GLWSKV VDEVGGEALGRLLVVYPWT+RFF+SFGDLST DAVMNNPK
Sbjct: 1  MVHLTGEKAAVTGLWSKVNVDVGGGALGRLLVVYPWTQRFDSFGDLSTPDVAVMNNPK 60

Query: 61  VKAHGSKVLNSFGDGLNHLNLDNLKGTAKLSELHCDKLHVDPENFRLLGNVLVVVLARHFG 120
          VKAHG KVLNSF +GL +LDNLKGT+AKLSELHCDKLHVDPENF+LLGNVLV VLA HFG
Sbjct: 61  VKAHGKKVLNSFSEGLKNLDNLKGTFAKLSELHCDKLHVDPENFKLLGNVLVCVLAHHFG 120

Query: 121 KEFTPDLQAAYQKVAVGVANALAHRYH 147
          KEFTP +QAAYQKVAVGVANALAH+YH
Sbjct: 121 KEFTPQVQAAYQKVAVGVANALAHKYH 147
```

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In case of problems, please read the online BLAST help.
If your question is not covered, please contact <helpdesk@expasy.org>.

NCBI BLAST program reference [PMID:9254694]:
Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402 (1997).

=====

Query: 222 AA (of which 7% low-complexity regions filtered out)
Date run: 2007-02-09 18:08:22 UTC+0100 on blast01.vital-it.ch
Program: NCBI BLASTP 2.2.15 [Oct-15-2006]
Database: UniProtKB Mammalia
240,475 sequences; 91,865,493 total letters
UniProt Knowledgebase Release 9.6 consists of:
UniProtKB/Swiss-Prot Release 51.6 of 06-Feb-2007: 257964 entries
UniProtKB/TrEMBL Release 34.6 of 06-Feb-2007: 3745801 entries

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List of potentially matching sequences

Send selected sequences to

☐ Include query sequence

	Db	AC	Description	Score	E-value
<input type="checkbox"/>	sp	O97943	CASA1_CAMDR Alpha-S1-casein precursor [CSN1S1] [Camelu...	418	e-117
<input type="checkbox"/>	sp	P39035	CASA1_PIG Alpha-S1-casein precursor [CSN1S1] [Sus scro...	176	8e-44
<input type="checkbox"/>	tr	Q95K27	_HORSE AlphaS1-casein [Equus caballus (Horse)]	146	5e-35
<input type="checkbox"/>	tr	Q8SPR1	_HORSE Alpha s1 casein [Equus caballus (Horse)]	146	5e-35
<input type="checkbox"/>	sp_vs	P04653-1	Isoform 2 of P04653 - Ovis aries (Sheep) [CSN1S1]...	134	3e-31
<input type="checkbox"/>	tr	Q8MIH4	_CAPHI Alpha s1 casein [csn1S1] [Capra hircus (Goat)]	131	2e-30
<input type="checkbox"/>	tr	Q69E26	_CAPHI CSCN1 [Capra hircus (Goat)]	130	4e-30
<input type="checkbox"/>	sp	P18626	CASA1_CAPHI Alpha-S1-casein precursor (Alpha-S1-CN) [C...	128	1e-29
<input type="checkbox"/>	sp	P04653	CASA1_SHEEP Alpha-S1-casein precursor [CSN1S1] [Ovis a...	127	3e-29
<input type="checkbox"/>	sp	P02662	CASA1_BOVIN Alpha-S1-casein precursor [CSN1S1] [Bos ta...	126	5e-29
<input type="checkbox"/>	sp_vs	P47710-2	Isoform 2 of P47710 - Homo sapiens (Human) [CSN1S...	126	5e-29
<input type="checkbox"/>	tr	A1A511	_HUMAN Casein alpha s1 [CSN1S1] [Homo sapiens (Human)]	124	2e-28
<input type="checkbox"/>	sp	O62823	CASA1_BUBBU Alpha-S1-casein precursor [CSN1S1] [Bubalu...	123	5e-28
<input type="checkbox"/>	sp	P47710	CASA1_HUMAN Alpha-S1-casein precursor [Contains: Casox...	123	6e-28
<input type="checkbox"/>	tr	A1A510	_HUMAN Casein alpha s1 (Casein alpha s1, isoform CRA_b)...	123	6e-28
<input type="checkbox"/>	tr	Q4F6X6	_BUBBU Alpha-S1 casein [Bubalus bubalis (Domestic water...	120	4e-27
<input type="checkbox"/>	tr	Q4PNR5	_HUMAN Casein [Homo sapiens (Human)]	120	5e-27
<input type="checkbox"/>	sp	P09115	CASA1_RABIT Alpha-S1-casein precursor (Alpha-casein) [...	119	9e-27
<input type="checkbox"/>	sp	P04656	CASA1_CAVPO Alpha-S1-casein precurscr (Casein-B) [CSN1...	116	7e-26
<input type="checkbox"/>	sp_vs	P47710-3	Isoform 3 of P47710 - Homo sapiens (Human) [CSN1S...	107	3e-23
<input type="checkbox"/>	sp	P02661	CASA1_RAT Alpha-S1-casein precursor (Alpha-casein) [Cs...	68	3e-11
<input type="checkbox"/>	tr	Q8MIH2	_CAPHI Alpha s1 casein [csn1S1] [Capra hircus (Goat)]	67	5e-11
<input type="checkbox"/>	tr	Q8MIH3	_CAPHI Alpha s1 casein [csn1S1] [Capra hircus (Goat)]	64	3e-10
<input type="checkbox"/>	sp	P19228	CASA1_MOUSE Alpha-S1-casein precursor (Alpha-casein) [...	62	1e-09
<input type="checkbox"/>	tr	Q99JM6	_MOUSE Csn1s1 protein [Csn1s1] [Mus musculus (Mouse)]	62	1e-09
<input type="checkbox"/>	tr	Q99M19	_MOUSE Csn1s1 protein [Csn1s1] [Mus musculus (Mouse)]	54	6e-07
<input type="checkbox"/>	tr	Q91VV1	_MOUSE Csn1s1 protein [Csn1s1] [Mus musculus (Mouse)]	50	8e-06
<input type="checkbox"/>	sp	P09116	CASB_RABIT Beta-casein precursor [CSN2] [Oryctolagus c...	39	0.015
<input type="checkbox"/>	sp	Q9GKK3	CASB_HORSE Beta-casein precursor [CSN2] [Equus caballu...	37	0.073
<input type="checkbox"/>	sp_vs	Q9GKK3-3	Isoform 3 of Q9GKK3 - Equus caballus (Horse) [CSN...	37	0.073
<input type="checkbox"/>	sp_vs	Q9GKK3-2	Isoform 2 of Q9GKK3 - Equus caballus (Horse) [CSN...	36	0.096

<input type="checkbox"/>	sp	P02666	CASB_BOVIN Beta-casein precursor [CSN2] [Bos taurus (B...]	35	0.21
<input type="checkbox"/>	tr	Q5EEQ7	_BOVIN Beta-casein (Fragment) [Bos taurus (Bovine)]	35	0.21
<input type="checkbox"/>	tr	Q5EEQ6	_BOVIN Kappa-casein (Fragment) [Bos taurus (Bovine)]	35	0.21
<input type="checkbox"/>	tr	Q2TA13	_BOVIN CSN2 protein [CSN2] [Bos taurus (Bovine)]	35	0.21
<input type="checkbox"/>	sp	Q9TSI0	CASB_BUBBU Beta-casein precursor [CSN2] [Bubalus bubal...]	35	0.28
<input type="checkbox"/>	sp	Q9TVD0	CASB_CAMDR Beta-casein precursor [CSN2] [Camelus drome...]	33	0.62
<input type="checkbox"/>	sp	P28550	CASB_MACEU Beta-casein precursor [CSN2] [Macropus euge...]	32	1.4
<input type="checkbox"/>	sp	P11839	CASB_SHEEP Beta-casein precursor [CSN2] [Ovis aries (S...]	32	1.8
<input type="checkbox"/>	sp	P39037	CASB_PIG Beta-casein precursor [CSN2] [Sus scrofa (Pig)]	32	1.8
<input type="checkbox"/>	tr	Q712N8	_CAPHI Beta-casein precursor [csn2] [Capra hircus (Goat)]	32	1.8
<input type="checkbox"/>	tr	Q7M2U6	_BOVIN Alpha-S1-casein (Fragments) [Bos taurus (Bovine)]	32	1.8
<input type="checkbox"/>	sp	Q9XSE4	CASB_TRIVU Beta-casein precursor [CSN2] [Trichosurus v...]	32	2.4
<input type="checkbox"/>	sp	Q9JM52	MINK1_MOUSE Misshapen-like kinase 1 (EC 2.7.11.1) (Mit...]	31	3.1
<input type="checkbox"/>	sp	Q8N4C8	MINK1_HUMAN Misshapen-like kinase 1 (EC 2.7.11.1) (Mit...]	31	3.1
<input type="checkbox"/>	sp	P33048	CASB_CAPHI Beta-casein precursor [CSN2] [Capra hircus ...]	31	3.1
<input type="checkbox"/>	tr	Q5SXF9	_MOUSE Mitogen-activated protein kinase kinase k...	31	3.1
<input type="checkbox"/>	tr	Q5SXG2	_MOUSE Mitogen-activated protein kinase kinase kinase k...	31	3.1
<input type="checkbox"/>	tr	Q5SXG1	_MOUSE Mitogen-activated protein kinase kinase kinase k...	31	3.1
<input type="checkbox"/>	tr	Q5SXG3	_MOUSE Mitogen-activated protein kinase kinase kinase k...	31	3.1
<input type="checkbox"/>	tr	Q5SXG0	_MOUSE Mitogen-activated protein kinase kinase kinase k...	31	3.1
<input type="checkbox"/>	tr	Q7TT13	_MOUSE Mink1 protein [Mink1] [Mus musculus (Mouse)]	31	3.1
<input type="checkbox"/>	tr	Q3SYJ2	_MOUSE 4930432K09Rik protein [4930432K09Rik] [Mus muscu...]	31	3.1
<input type="checkbox"/>	tr	Q3SZ11	_BOVIN Similar to replication protein A3, 14kDa [MGC128...]	31	3.1
<input type="checkbox"/>	tr	A0JEQ3	_CAPHI Beta-casein precursor [csn2] [Capra hircus (Goat)]	31	3.1
<input type="checkbox"/>	tr	Q95L76	_CAPHI Beta-casein precursor [csn2] [Capra hircus (Goat)]	31	3.1
<input type="checkbox"/>	tr	Q5U820	_HUMAN Misshapen/NIKs-related kinase isoform beta [MINK...]	31	3.1
<input type="checkbox"/>	sp_vs	Q8N4C8-2	Isoform 1 of Q8N4C8 - Homo sapiens (Human) [MINK1...]	31	3.1
<input type="checkbox"/>	sp_vs	Q8N4C8-3	Isoform 2 of Q8N4C8 - Homo sapiens (Human) [MINK1...]	31	3.1
<input type="checkbox"/>	sp_vs	Q9JM52-2	Isoform 1 of Q9JM52 - Mus musculus (Mouse) [Mink1...]	31	3.1
<input type="checkbox"/>	sp_vs	Q9JM52-3	Isoform 3 of Q9JM52 - Mus musculus (Mouse) [Mink1...]	31	3.1
<input type="checkbox"/>	tr	Q9N2G8	_CANFA Beta-casein [Canis familiaris (Dog)]	31	4.0
<input type="checkbox"/>	sp	P50419	CASA2_RABIT Alpha-S2-casein precursor (Alpha-S2B-casei...]	30	5.2
<input type="checkbox"/>	tr	Q9D9N6	_MOUSE Adult male testis cDNA, RIKEN full-length enrich...	30	5.2
<input type="checkbox"/>	tr	Q9CVP0	_MOUSE Adult male testis cDNA, RIKEN full-length enrich...	30	5.2
<input type="checkbox"/>	tr	Q5SRE0	_MOUSE Aldehyde dehydrogenase family 3, subfamily A2 [A...]	30	6.8
<input type="checkbox"/>	tr	Q9XSE3	_TRIVU Alpha-casein [Trichosurus vulpecula (Brush-tail...]	30	6.8
<input type="checkbox"/>	sp	P28549	CASA1_MACEU Alpha-S1-casein precursor (Alpha-casein) [...]	30	8.9

Graphical overview of the alignments

[Click here](#) to resubmit your query after masking regions matching PROSITE profiles or Pfam HMMs
(🔗 Help) (use ScanProsite for more details about PROSITE matches)

Profile hits

Pfam hits

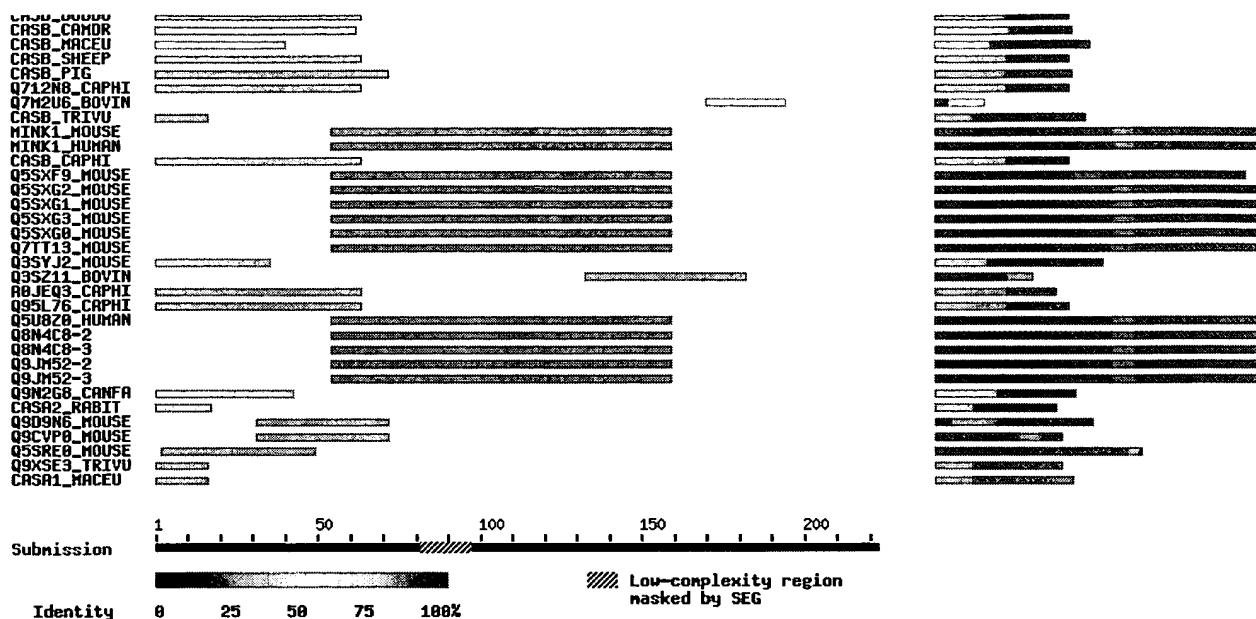
Submission

Matches on query sequence

CASA1_CAMDR
CASA1_PIG
Q9SKZ7_HORSE
Q8SPR1_HORSE
P04653-1
Q8MIH4_CAPHI
Q69EZ6_CAPHI
CASA1_CAPHI
CASA1_SHEEP
CASA1_BOVIN
P47718-2
A1A511_HUMAN
CASA1_BUBBU
CASA1_HUMAN
A1A518_HUMAN
Q4F6X8_BUBBU
Q4PNR5_HUMAN
CASA1_RABIT
CASA1_CAVPO
P47718-3
CASA1_RAT
Q8MIH2_CAPHI
Q8MIH3_CAPHI
CASA1_MOUSE
Q99JM6_MOUSE
Q99M19_MOUSE
Q91VY1_MOUSE
CASB_RABIT
CASB_HORSE
Q9GKK3-3
Q9GKK3-2
CASB_BOVIN
Q5EEQ7_BOVIN
Q5EEQ6_BOVIN
Q2TA13_BOVIN
P28549

Matches on hit sequences (sort scale)

1 100 200 400 600 800 1345



Alignments

sp 097943 Alpha-S1-casein precursor [CSN1S1] [Camelus dromedarius (Dromedary)] 222 AA
CASB1_CAMD (Arabian camel) align

Score = 418 bits (1074), Expect = e-117
Identities = 206/222 (92%), Positives = 206/222 (92%)

Query: 1 MKLLILTCLVAVALARPKYPLRYPEVFQNEPDSIEEVLNKRKILELAVVSPIQFRQENID 60
MKLLILTCLVAVALARPKYPLRYPEVFQNEPDSIEEVLNKRKILELAVVSPIQFRQENID
Sbjct: 1 MKLLILTCLVAVALARPKYPLRYPEVFQNEPDSIEEVLNKRKILELAVVSPIQFRQENID 60

Query: 61 ELKDRNEPTEDHIMEDTERKXXXXXXXXXXXXXQDKILKEDMPSQRYLEELHRLNK 120
ELKDRNEPTEDHIMEDTERK QDKILKEDMPSQRYLEELHRLNK
Sbjct: 61 ELKDRNEPTEDHIMEDTERKESGSSSSEEVVSSTTEQDKILKEDMPSQRYLEELHRLNK 120

Query: 121 YKLLQLEAIRDQKLIIPRVKLSHPYLEQLYRINEDNHPQLGEPVKVVTQPPFPFQLGAS 180
YKLLQLEAIRDQKLIIPRVKLSHPYLEQLYRINEDNHPQLGEPVKVVTQPPFPFQLGAS
Sbjct: 121 YKLLQLEAIRDQKLIIPRVKLSHPYLEQLYRINEDNHPQLGEPVKVVTQPPFPFQLGAS 180

Query: 181 PYVAWYPPQVMQYIAHPSSYDTPEGIASEDGGKTDVMPQWW 222
PYVAWYPPQVMQYIAHPSSYDTPEGIASEDGGKTDVMPQWW
Sbjct: 181 PYVAWYPPQVMQYIAHPSSYDTPEGIASEDGGKTDVMPQWW 222

sp P39035 Alpha-S1-casein precursor [CSN1S1] [Sus scrofa (Pig)] 206 AA
CASB1_PIG align

Score = 176 bits (445), Expect = 8e-44
Identities = 110/231 (47%), Positives = 128/231 (55%), Gaps = 35/231 (15%)

Query: 1 MKLLILTCLVAVALARPKYPLRYPEVFQNEPDSIEEVLNKRKILELAVVSPIQFRQENI 59
MKLLI CL AVALARPK PLR+ E QNEPDS EE+ +RK L V + QFRQE I
Sbjct: 1 MKLLIFICLAAVALARPKPLRHQHLQNEPDSREELFKERKFLRFPEVPLLSQFRQEII 60

Query: 60 DELKDRNEPTEDHIMEDTERKXXXXXXXXXXXXXQDKILK-EDMPSQRYLEELHRL 118
+EL +H ME E++ QK + K ED+PSQ YL L L
Sbjct: 61 NEL-----NRNHGMEGHEQRGSSSSSEEVVGNASAEQKHVQKEEDVPSQSYLGHLQGL 113

Query: 119 NKYKLLQLEAIRDQKLIIPRVKLSHPYLEQLYRINEDNHPQLGEPVKVVTQ-----P 170
NKYKL QLEAI DQ +L+R NED H Q GEP+K V Q P
Sbjct: 114 NKYKLRQLEAIHQD-----ELHRTNEDKHTQQGEPKMGVNGEQAYFYFEP 158

Query: 171 FPQFFQLGASPYVAWYPPQVMQYIAHPSSYDTPEGIASEDGGKTDVMPQW 221
QF+QL A PY WYYP YIAHP + P+ A E GGKT+MPQW
Sbjct: 159 LHQFYQLDAYPYATWYYP---QYIAHPLFTNIPQTAPEKGGKTEIMPQW 206

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NCBI BLAST program reference [PMID:9254694]:
Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

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Query: 232 AA
Date run: 2007-02-09 18:11:58 UTC+0100 on blast01.vital-it.ch
Program: NCBI BLASTP 2.2.15 [Oct-15-2006]
Database: UniProtKB Mammalia
240,475 sequences; 91,865,493 total letters
UniProt Knowledgebase Release 9.6 consists of:
UniProtKB/Swiss-Prot Release 51.6 of 06-Feb-2007: 257964 entries
UniProtKB/TrEMBL Release 34.6 of 06-Feb-2007: 3745801 entries

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List of potentially matching sequences

Send selected sequences to

☐ Include query sequence

Db	AC	Description	Score	E-value
<input type="checkbox"/>	sp	Q9TVD0 CASB_CAMDR Beta-casein precursor [CSN2] [Camelus drome...	463	e-130
<input type="checkbox"/>	sp	P39037 CASB_PIG Beta-casein precursor [CSN2] [Sus scrofa (Pig)]	305	7e-83
<input type="checkbox"/>	tr	Q28229 _CAMDR B-casein (Fragment) [Camelus dromedarius (Dromed...	286	4e-77
<input type="checkbox"/>	sp	P11839 CASB_SHEEP Beta-casein precursor [CSN2] [Ovis aries (S...	285	7e-77
<input type="checkbox"/>	sp	Q9TSI0 CASB_BUBBU Beta-casein precursor [CSN2] [Bubalus bubal...	285	1e-76
<input type="checkbox"/>	tr	Q712N8 _CAPHI Beta-casein precursor [csn2] [Capra hircus (Goat)]	282	6e-76
<input type="checkbox"/>	tr	Q95L76 _CAPHI Beta-casein precursor [csn2] [Capra hircus (Goat)]	282	6e-76
<input type="checkbox"/>	sp	P33048 CASB_CAPHI Beta-casein precursor [CSN2] [Capra hircus ...	281	1e-75
<input type="checkbox"/>	sp	P02666 CASB_BOVIN Beta-casein precursor [CSN2] [Bos taurus (B...	281	2e-75
<input type="checkbox"/>	tr	Q9N2G8 _CANFA Beta-casein [Canis familiaris (Dog)]	280	4e-75
<input type="checkbox"/>	tr	Q2TA13 _BOVIN CSN2 protein [CSN2] [Bos taurus (Bovine)]	277	3e-74
<input type="checkbox"/>	sp	P05814 CASB_HUMAN Beta-casein precursor [CSN2] [Homo sapiens ...	268	1e-71
<input type="checkbox"/>	sp	Q9GKK3 CASB_HORSE Beta-casein precursor [CSN2] [Equus caballu...	256	4e-68
<input type="checkbox"/>	sp_vs	Q9GKK3-2 Isoform 2 of Q9GKK3 - Equus caballus (Horse) [CSN...	241	2e-63
<input type="checkbox"/>	tr	A0JEQ3 _CAPHI Beta-casein precursor [csn2] [Capra hircus (Goat)]	237	2e-62
<input type="checkbox"/>	sp	P09116 CASB_RABIT Beta-casein precursor [CSN2] [Oryctolagus c...	222	1e-57
<input type="checkbox"/>	tr	P79231 _PHYCA Beta casein (Fragment) [Physeter catodon (Sperm ...	207	3e-53
<input type="checkbox"/>	tr	Q6PKV3 _BUBBU Beta casein (Fragment) [Bubalus bubalis (Domesti...	205	1e-52
<input type="checkbox"/>	tr	A1E9C8 _BUBBU Beta-casein (Fragment) [CSN2] [Bubalus bubalis (...	202	1e-51
<input type="checkbox"/>	tr	Q27953 _BALPH B-casein (Fragment) [Balaenoptera physalus (Finb...	201	1e-51
<input type="checkbox"/>	tr	A1YT08 _BOSIN Beta-casein (Fragment) [CSN2] [Bos indicus (Zebu)]	198	1e-50
<input type="checkbox"/>	tr	Q3HW31 _BUBBU Beta-casein (Fragment) [beta-casein] [Bubalus bu...	196	6e-50
<input type="checkbox"/>	tr	Q3HW30 _BUBBU Beta-casein (Fragment) [beta-casein] [Bubalus bu...	196	6e-50
<input type="checkbox"/>	tr	Q28355 _DELLE B-casein (Fragment) [Delphinapterus leucas (Belu...	196	6e-50
<input type="checkbox"/>	tr	A1YQZ8 _BOVIN Beta-casein (Fragment) [CSN2] [Bos taurus (Bovine)]	195	1e-49
<input type="checkbox"/>	tr	Q29151 _UNCUN B-casein (Fragment) [Uncia uncia (Snow leopard) ...	181	3e-45
<input type="checkbox"/>	tr	Q27939 _CETA B-casein (Fragment) [Alces alces (moose)]	179	6e-45
<input type="checkbox"/>	tr	Q28418 _GIRCA B-casein (Fragment) [Giraffa camelopardalis (Gir...	179	1e-44
<input type="checkbox"/>	tr	Q27938 _ANTAM B-casein (Fragment) [Antilocapra americana (Pron...	178	2e-44
<input type="checkbox"/>	tr	Q9BDG5 _BOVIN Beta casein B (Fragment) [bCN B] [Bos taurus (Bo...	176	6e-44
<input type="checkbox"/>	tr	Q29139 _TRANA B-casein (Fragment) [Tragulius napu (Balabac chev...	172	1e-42

<input type="checkbox"/>	tr	P79092	_AIFU Beta casein (Fragment) [Ailurus fulgens (Lesser ...	161	2e-39
<input type="checkbox"/>	tr	Q28401	_EUGR B-casein (Fragment) [Equus grevyi (Grevy's zebra)]	160	4e-39
<input type="checkbox"/>	tr	Q29136	_TAPIN B-casein (Fragment) [Tapirus indicus (Asiatic ta...	159	8e-39
<input type="checkbox"/>	tr	Q28442	_HIPAM B-casein (Fragment) [Hippopotamus amphibius (Hip...	149	6e-36
<input type="checkbox"/>	sp	P10598	CASB_MOUSE Beta-casein precursor [Csn2] [Mus musculus ...	141	2e-33
<input type="checkbox"/>	tr	Q3TP33	_MOUSE 10 days lactation, adult female mammary gland cD...	141	2e-33
<input type="checkbox"/>	tr	Q8BGL0	_MOUSE 10 days lactation, adult female mammary gland cD...	135	2e-31
<input type="checkbox"/>	tr	Q9TSD5	_BOVIN Beta-casein A2 variant (Fragments) [Bos taurus (...	134	2e-31
<input type="checkbox"/>	tr	A0N0S5	_BUBBU Beta-casein (Fragment) [Bubalus bubalis (Domesti...	133	6e-31
<input type="checkbox"/>	sp	P02665	CASB_RAT Beta-casein precursor [Csn2] [Rattus norvegic...	131	2e-30
<input type="checkbox"/>	tr	Q5YD57	_CAPHI Beta-casein (Fragment) [CSN2] [Capra hircus (Goat)]	128	2e-29
<input type="checkbox"/>	tr	Q5EEQ7	_BOVIN Beta-casein (Fragment) [Bos taurus (Bovine)]	119	7e-27
<input type="checkbox"/>	tr	Q5EEQ6	_BOVIN Kappa-casein (Fragment) [Bos taurus (Bovine)]	110	6e-24
<input type="checkbox"/>	tr	Q28795	_TAYTA B-casein (Fragment) [Tayassu tajacu (Collared pe...	91	3e-18
<input type="checkbox"/>	sp_vs	Q9GKK3-3	Isoform 3 of Q9GKK3 - Equus caballus (Horse) [CSN...	78	3e-14
<input type="checkbox"/>	tr	Q6UN62	_BOSIN Beta-casein variant A2' (Fragment) [Bos indicus ...	73	8e-13
<input type="checkbox"/>	tr	Q6UN63	_BOVIN Beta-casein variant I (Fragment) [Bos taurus (Bo...	72	2e-12
<input type="checkbox"/>	tr	Q155X6	_BOSIN Beta casein (Fragment) [Bos indicus (Zebu)]	65	2e-10
<input type="checkbox"/>	tr	Q155X5	_BOSIN Beta casein (Fragment) [Bos indicus (Zebu)]	63	8e-10
<input type="checkbox"/>	tr	Q7M2U5	_BUBBU Beta-casein (Fragment) [Bubalus bubalis (Domesti...	57	7e-08
<input type="checkbox"/>	sp	Q8WZ42	TITIN_HUMAN Titin (EC 2.7.11.1) (Connectin) [Rhabdomyo...	53	8e-07
<input type="checkbox"/>	sp_vs	Q8WZ42-2	Isoform 2 of Q8WZ42 - Homo sapiens (Human) [TTN] ...	53	8e-07
<input type="checkbox"/>	sp_vs	Q8WZ42-4	Isoform 4 of Q8WZ42 - Homo sapiens (Human) [TTN] ...	53	8e-07
<input type="checkbox"/>	sp_vs	Q8WZ42-7	Isoform 7 of Q8WZ42 - Homo sapiens (Human) [TTN] ...	53	8e-07
<input type="checkbox"/>	sp_vs	Q8WZ42-8	Isoform 8 of Q8WZ42 - Homo sapiens (Human) [TTN] ...	53	8e-07
<input type="checkbox"/>	tr	Q9UCM5	_HUMAN Beta-casein (Fragment) [Homo sapiens (Human)]	53	1e-06
<input type="checkbox"/>	sp	P02817	AMELX_BOVIN Amelogenin, X isoform precursor (Class I a...	52	1e-06
<input type="checkbox"/>	tr	Q861X2	_BOVIN Amelogenin (Fragment) [AMELX] [Bos taurus (Bovine)]	52	1e-06
<input type="checkbox"/>	tr	Q3UH66	_MOUSE cDNA, RIKEN full-length enriched library, clone:...	50	9e-06
<input type="checkbox"/>	tr	Q9JLE9	_RAT GABA-A receptor epsilon-like subunit [Epsilon] [Ra...	49	1e-05
<input type="checkbox"/>	sp_vs	Q8WZ42-5	Isoform 5 of Q8WZ42 - Homo sapiens (Human) [TTN] ...	49	1e-05
<input type="checkbox"/>	tr	Q71S18	_HUMAN Titin (Fragment) [TTN] [Homo sapiens (Human)]	49	2e-05
<input type="checkbox"/>	tr	Q35745	_MOUSE Zinc finger protein [Plagl1] [Mus musculus (Mouse)]	48	3e-05
<input type="checkbox"/>	tr	Q3UQR2	_MOUSE 13 days embryo heart cDNA, RIKEN full-length enr...	48	3e-05
<input type="checkbox"/>	tr	Q9JLQ4	_MOUSE Zinc finger protein ZAC1 [Plagl1] [Mus musculus ...	48	3e-05
<input type="checkbox"/>	tr	Q3UQW2	_MOUSE 12 days embryo eyeball cDNA, RIKEN full-length e...	48	3e-05
<input type="checkbox"/>	tr	Q811F2	_MOUSE Wnk2 protein (Fragment) [Wnk2] [Mus musculus (Mo...	47	8e-05
<input type="checkbox"/>	tr	Q8WMK6	_CAPCR Amelogenin X (Fragment) [AMELX] [Capricornis cri...	47	8e-05
<input type="checkbox"/>	sp	Q6PB44	PTN23_MOUSE Tyrosine-protein phosphatase non-receptor ...	46	1e-04
<input type="checkbox"/>	tr	Q8NBB9	_HUMAN cDNA FLJ33731 fis, clone BRAWH2017685, moderatel...	46	1e-04
<input type="checkbox"/>	sp_vs	Q6PB44-2	Isoform 2 of Q6PB44 - Mus musculus (Mouse) [Ptpn2...	46	1e-04
<input type="checkbox"/>	tr	Q18P50	_HUMAN Zinc finger homeobox protein 4 (ZFH-4) [ZFH-4] [...	46	1e-04
<input type="checkbox"/>	tr	Q8NFA5	_HUMAN FLJ00353 protein (Fragment) [FLJ00353] [Homo sap...	45	2e-04
<input type="checkbox"/>	tr	Q86YA8	_HUMAN YLPM1 protein (Fragment) [YLPM1] [Homo sapiens (...	45	2e-04
<input type="checkbox"/>	tr	Q8CHI3	_MOUSE MKIAA0054 protein (Fragment) [Helz] [Mus musculu...	45	2e-04
<input type="checkbox"/>	tr	Q6DFV5	_MOUSE Helicase with zinc finger domain [Helz] [Mus mus...	45	2e-04
<input type="checkbox"/>	tr	Q8BZ26	_MOUSE 15 days embryo male testis cDNA, RIKEN full-leng...	45	2e-04
<input type="checkbox"/>	tr	Q7YRG0	_CANFA Cardiac titin isoform N2BA (Fragment) [TTN] [Can...	45	2e-04
<input type="checkbox"/>	sp	P42694	HELZ_HUMAN Probable helicase with zinc-finger domain (...	45	3e-04
<input type="checkbox"/>	tr	Q9JLE8	_MOUSE GABA-A receptor epsilon-like subunit [Gabre] [Mu...	45	3e-04
<input type="checkbox"/>	tr	Q9JLE7	_MOUSE GABA-A receptor epsilon-like subunit [Gabre] [Mu...	45	3e-04
<input type="checkbox"/>	tr	Q861X3	_OTOGA Amelogenin (Fragment) [AMELX] [Otolemur garnetti...	45	3e-04
<input type="checkbox"/>	tr	A1L4L4	_HUMAN Helicase with zinc finger [HELZ] [Homo sapiens (...	45	3e-04
<input type="checkbox"/>	tr	Q86UP3	_HUMAN Zinc finger homeodomain 4 protein [ZFXH4] [Homo ...	45	3e-04
<input type="checkbox"/>	sp_vs	Q8CGF7-2	Isoform 2 of Q8CGF7 - Mus musculus (Mouse) [Tcerg...	45	3e-04
<input type="checkbox"/>	tr	Q861X5	_LEMCA Amelogenin (Fragment) [AMELX] [Lemur catta (Ring...	44	4e-04
<input type="checkbox"/>	tr	Q8WU72	_HUMAN CIZ1 protein (CDKN1A interacting zinc finger pro...	44	4e-04
<input type="checkbox"/>	tr	Q5SYW3	_HUMAN CDKN1A interacting zinc finger protein 1 (CDKN1A...	44	4e-04
<input type="checkbox"/>	tr	Q9H868	_HUMAN cDNA FLJ13916 fis, clone Y79AA1000342, moderatel...	44	4e-04
<input type="checkbox"/>	sp	Q9XSE4	CASB_TRIVU Beta-casein precursor [CSN2] [Trichosurus v...	44	5e-04
<input type="checkbox"/>	sp	Q60885	BRD4_HUMAN Bromodomain-containing protein 4 (HUNK1 pro...	43	8e-04
<input type="checkbox"/>	tr	Q3UH70	_MOUSE 14 days pregnant adult female placenta cDNA, RIK...	43	8e-04
<input type="checkbox"/>	sp	Q9ESU6	BRD4_MOUSE Bromodomain-containing protein 4 (Mitotic c...	43	0.001
<input type="checkbox"/>	tr	Q7YRG2	_CANFA Cardiac titin isoform N2BA (Fragment) [TTN] [Can...	43	0.001
<input type="checkbox"/>	tr	Q7YRG1	_CANFA Cardiac titin isoform N2BA (Fragment) [TTN] [Can...	43	0.001
<input type="checkbox"/>	tr	Q7YRPF5	_CANFA Cardiac titin (Fragment) [TTN] [Canis familiaris...	43	0.001

☐ sp Q6R0H6 ALEX_MOUSE Protein ALEX (Alternative gene product enco... 42 0.001
☐ tr Q7YRF9 _CANFA Cardiac titin isoform N2BA (Fragment) [TTN] [Can... 42 0.001
☐ sp P79149 PININ_CANFA Pinin [PNN] [Canis familiaris (Dog)] 42 0.002

Graphical overview of the alignments

[Click here](#) to resubmit your query after masking regions matching PROSITE profiles or Pfam HMMs
([Help](#)) (use ScanProsite for more details about PROSITE matches)

Profile hits

Pfam hits

Submission

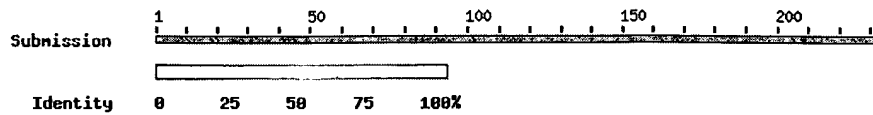
CASB_CAMDR
CASB_PIG
Q28229_CAMDR
CASB_SHEEP
CASB_BUBBU
Q71288_CAPHI
Q95L76_CAPHI
CASB_CAPHI
CASB_BOVIN
Q9N268_CANFA
Q2TA13_BOVIN
CASB_HUMAN
CASB_HORSE
Q9GKK3-2
A6JEQ3_CAPHI
CASB_RABIT
P79231_PHYCA
Q6PKV3_BUBBU
A1E9C8_BUBBU
Q27953_BALPH
A1YT88_BOVIN
Q3HM31_BUBBU
Q3HM30_BUBBU
Q28355_DELE
A1YQ28_BOVIN
Q29151_UNCUM
Q27939_QCYTA
Q28418_GIRCA
Q27938_ANTAM
Q98065_BOVIN
Q29139_TRANA
P79892_AILFU
Q28401_EQUGR
Q29136_TAPIN
Q28442_HIPAM
CASB_MOUSE
Q3TP33_MOUSE
Q88G18_MOUSE
Q9TSD5_BOVIN
A8N8S5_BUBBU
CASB_RAT
Q5YD57_CAPHI
Q5EEQ7_BOVIN
Q5EEQ6_BOVIN
Q28795_TAYTA
Q9GKK3-3
Q6UN62_BOVIN
Q6UN63_BOVIN
Q155X6_BOVIN
Q155X5_BOVIN
Q7H2U5_BUBBU
TITIN_HUMAN
Q8NZ42-2
Q8NZ42-4
Q8NZ42-7
Q8NZ42-8
Q9UCH5_HUMAN
AMELX_BOVIN
Q861X2_BOVIN
Q3UH66_MOUSE
Q9JLE9_RAT
Q8NZ42-5
Q71518_HUMAN
Q35745_MOUSE
Q3UQR2_MOUSE
Q9JLQ4_MOUSE
Q3UQH2_MOUSE
Q811F2_MOUSE
Q84MK6_CACPR
PTN23_MOUSE
Q8NBB9_HUMAN
Q6PB44-2
Q18PS8_HUMAN
Q8NF45_HUMAN
Q86YA8_HUMAN
Q8CHI3_MOUSE
Q6DFV5_MOUSE
Q8BZ26_MOUSE
Q7YRG8_CANFA
HEL2_HUMAN
Q9JLE8_MOUSE
Q9JLE7_MOUSE
Q861X3_OTOGA
A1L4L4_HUMAN
Q86UP3_HUMAN
Q8CGF7-2
Q861X5_LEMCA
Q84U72_HUMAN
Q55YN3_HUMAN
Q8H868_HUMAN
CASB_TRLVI
BRD4_HUMAN
Q3UH78_MOUSE
BRD4_MOUSE
Q7YRG2_CANFA
Q7YRG1_CANFA
Q7YRF5_CANFA
ALEX_MOUSE
Q7YRF9_CANFA
PININ_CANFA

Matches on query sequence

1 50 100 150 200

Matches on hit sequences (sqrt scale)

1 1000 3000 6000 10000 17000 34474



Alignments

sp Q9TVD0 Beta-casein precursor [CSN2] [Camelus dromedarius (Dromedary)] 232 AA
CASB_CAMDR (Arabian camel)] align

Score = 463 bits (1192), Expect = e-130
Identities = 232/232 (100%), Positives = 232/232 (100%)

Query: 1 MKVLILACRVALALAREKEEFKTAGEALESISSEESITHINKQKIEKFKEEQQTETE 60
MKVLILACRVALALAREKEEFKTAGEALESISSEESITHINKQKIEKFKEEQQTETE
Sbjct: 1 MKVLILACRVALALAREKEEFKTAGEALESISSEESITHINKQKIEKFKEEQQTETE 60

Query: 61 QQDKIYTFPQPQSLVYSHTPIYPILPQNFLPPLQPAVMVPFLQPKVMDVPKTKETIIP 120
QQDKIYTFPQPQSLVYSHTPIYPILPQNFLPPLQPAVMVPFLQPKVMDVPKTKETIIP
Sbjct: 61 QQDKIYTFPQPQSLVYSHTPIYPILPQNFLPPLQPAVMVPFLQPKVMDVPKTKETIIP 120

Query: 121 KRKEMPLLQSPVVPFTESQSLTLTDLENLHLPLPLQLSLMYQIPQVPQTPMIPPQSLLS 180
KRKEMPLLQSPVVPFTESQSLTLTDLENLHLPLPLQLSLMYQIPQVPQTPMIPPQSLLS
Sbjct: 121 KRKEMPLLQSPVVPFTESQSLTLTDLENLHLPLPLQLSLMYQIPQVPQTPMIPPQSLLS 180

Query: 181 LSQFKVLPVPQQMVPYPQRAMPVQAVLPFQEPVPDPVRGLHPVPQPLVPVIA 232
LSQFKVLPVPQQMVPYPQRAMPVQAVLPFQEPVPDPVRGLHPVPQPLVPVIA
Sbjct: 181 LSQFKVLPVPQQMVPYPQRAMPVQAVLPFQEPVPDPVRGLHPVPQPLVPVIA 232

sp P39037 Beta-casein precursor [CSN2] [Sus scrofa (Pig)] 232 AA
CASB_PIG align

Score = 305 bits (782), Expect = 7e-83
Identities = 156/230 (67%), Positives = 183/230 (79%), Gaps = 2/230 (0%)

Query: 1 MKVLILACRVALALAREKEEFKTAGEALESISSEESITHINKQKIEKFKEEQQTETE 60
MK+LILAC VALALAR KEE +GE +ES+SSSEESITHI+K+KIEK K EEQQQTE+E
Sbjct: 1 MKLLILACFVALALARAKEELNASGETVESLSSEESITHISKEKIEKLKREEQQQTENE 60

Query: 61 QQDKIYTFPQPQSLVYSHTPIYPILPQNFLPPLQPAVMVPFLQPKVMDVPKTKETIIP 120
+Q+KI+ FPQPQ L + +TEPIYPILPQN LP Q V+VP L P+VM K KETI+P
Sbjct: 61 RQNKIHQPQPQPLAHPYTEPIYPILPQNILPLAQVVPVVVLLHPEVMKDSKAKETIVP 120

Query: 121 KRKEMPLLQSPVVPFTESQSLTLTDLENLHLPLPLQLSLMYQIPQVPQTPMIPPQSLLS 180
KRK MP +SP PF E QSLTLTD E L LPLQLSLM+QIPQVPQTPM PQ LLS
Sbjct: 121 KRKGMFPFKSPAEPFVEGQSLTLTDFE--VLSLPLQLSLMHQIPQVPQTPMFPAPQPLLS 178

Query: 181 LSQFKVLPVPQQMVPYPQRAMPVQAVLPFQEPVPDPVRGLHPVPQPLVPV 230
L Q KVLVPVQQ+VP+PQR MP QA+L +Q+P+ P++G +PVPQP+ PV
Sbjct: 179 LPQAKVLPVPQQVVPFPQRDMPFQALLLYQDPLLGPLQGFYVPVPQPVAPV 228

tr Q28229 B-casein (Fragment) [Camelus dromedarius (Dromedary)] (Arabian camel)] 141 AA
Q28229_CAMDR align

Score = 286 bits (732), Expect = 4e-77
Identities = 140/141 (99%), Positives = 140/141 (99%)

Query: 65 IYTFPQPQSLVYSHTPIYPILPQNFLPPLQPAVMVPFLQPKVMDVPKTKETIIPKRKE 124
IYTFPQPQSLVYSHTPIYPILPQNFLPPLQPAVMVPFLQPKVMDVPKTKETIIPKRKE
Sbjct: 1 IYTFPQPQSLVYSHTPIYPILPQNFLPPLQPAVMVPFLQPKVMDVPKTKETIIPKRKE 60

Query: 125 MPLLQSPVVPFTESQSLTLTDLENLHLPLPLQLSLMYQIPQVPQTPMIPPQSLLSLSQF 184
MPLLQSPVVPFTESQSLTLTDLENLHLPLPLQLSLMYQIPQ PQTPIPPQSLLSLSQF
Sbjct: 61 MPLLQSPVVPFTESQSLTLTDLENLHLPLPLQLSLMYQIPQXPQTPMIPPQSLLSLSQF 120

Query: 185 KVLVPVQQMVPYPQRAMPVQA 205
KVLVPVQQMVPYPQRAMPVQA
Sbjct: 121 KVLVPVQQMVPYPQRAMPVQA 141